

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:08:53 ; Search time 68.1863 seconds
(without alignments)
1877.123 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGLVQPGSRL.....MHEALHNHYTQKLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	453	2 AAR33311	Humanised
2	2432	100.0	453	2 AAY85199	Heavy cha
3	2391	98.3	451	2 AA95659	Mus muscu
4	2391	98.3	451	2 AA95661	Mus muscu
5	2391	98.3	451	3 AAY85201	Light cha
6	2391	98.3	451	4 AAB47088	Anti-IgE
7	2391	98.3	451	4 AAB76948	Full leng
8	2391	98.3	451	4 AAB76950	Full leng
9	2369	97.4	451	2 AA95663	Mus muscu
10	2369	97.4	451	2 AAY50031	Human e27
11	2369	97.4	451	3 AAB07473	Amino aci
12	2369	97.4	451	4 AAB76952	Full leng
13	2369	97.4	451	4 AAB74212	E27 anti-
14	2369	97.4	451	6 AAB62798	E27 anti-
15	2214.5	91.1	452	2 AAY29458	Recombina
16	2214.5	91.1	452	3 AAY77766	Humanised
17	2214.5	91.1	452	3 AAB30322	Humanised
18	2214.5	91.1	452	6 ABU13799	Humanised
19	2214.5	91.1	452	6 ABU59512	Humanised
20	2214.5	91.1	452	7 AA93094	Protein #
21	2210	90.9	476	5 ABB81110	Anti-VEGF
22	2207.5	90.8	447	6 AAE33522	Human AOC
23	2205.5	90.7	452	4 AA69316	Anti-IL-8
24	2204.5	90.6	477	4 AAU14288	Human nov
25	2202.5	90.6	445	6 AAO31101	Human A2-

26	2201.5	90.5	447	6 AAE33523	Aae33523 Human AOC
27	2197.5	90.4	447	6 AAE33524	Aae33524 Human AOC
28	2191	90.1	449	6 ABE58273	Abp58273 Humanised
29	2191	90.1	468	6 ABE58275	Abp58275 Humanised
30	2183.5	89.8	475	2 AAR20057	Aar20057 Heavy cha
31	2182	89.7	449	3 AAY68810	Aay68810 A rat hea
32	2179.5	89.6	449	7 ADB85320	Adb85320 Heavy cha
33	2178	89.6	474	5 AAO14065	Aao14065 Heavy mon
34	2178	89.6	474	6 ABU08017	Abu08017 Human mon
35	2177.5	89.5	444	6 AAE35327	Aae35327 Humanised
36	2177.5	89.5	444	6 AAE34876	Aae34876 BWA4/8 a
37	2177	89.5	451	4 AAE12715	Aae12715 Human rec
38	2177	89.5	451	6 ABU58807	Abu58807 Mucin 1 (
39	2176.5	89.5	442	6 ABR39465	AbR39465 Humanised
40	2176.5	89.5	442	6 ABU08311	Abu08311 Humanised
41	2176.5	89.5	442	6 ABB80109	Abb80109 Heavy cha
42	2176.5	89.5	461	4 AAU07745	Aau07745 Humanised
43	2176.5	89.5	461	6 ABR39844	AbR39844 Hu266 N56
44	2176.5	89.5	461	6 ABR39847	AbR39847 Hu266 N56
45	2176.5	89.5	461	6 ABR39843	AbR39843 Hu266 N56

ALIGNMENTS

RESULT 1
AAR33311
ID AAR33311 standard; protein; 453 AA.

AC AAR33311;
DT 25-MAR-2003 (revised)
DT 05-JUL-1993 (first entry)
XX Humanised MaE11 Version 1 (intact IgG) heavy chain.
XX Antibody; high affinity; FCBH; low affinity; FCBL; IgE receptor;
XX histamine; mast cell; basophil; Kabat; CDR; murine; MaE11; Fab;
XX humael1v1.
OS Synthetic.
XX WO9304173-A1.
PN 04-MAR-1993.
PD 14-AUG-1992; 92WO-US006860.
PF 14-AUG-1991; 91US-00744768.
PR 07-MAY-1992; 92US-00879495.
XX (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
XX WPI; 1993-094004/11.
XX Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE
XX antagonists; useful for treating and preventing IgE-mediated disorders
XX e.g. allergies.
XX Example 4; Fig 3; 113pp; English.
XX Residues were selected from MaE11 and inserted or substituted into a
XX human Fab antibody background (Vh region Kabat subgroup III and VI region
XX kappa subgroup I). A first version, humael1v1 or version 1 is given
XX below. The affinity of version 1 was assayed and found to be ca. 100
XX times lower than that of the donor antibody MaE11. Therefore, further
XX modifications in the sequence of version 1 were made. (Updated on 25-MAR-
XX 2003 to correct PN field.)
SQ Sequence 453 AA;

Query Match 100.0%; Score 2432; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.6e-142; Indels 0; Gaps 0;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSINY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSINY 60

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAIVYCARGSHYFGHWHFAVWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAIVYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180
DB 121 SASTKGKPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180

QY 181 QSSGLYSLSVTVPSSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVITLPPS 240
DB 181 QSSGLYSLSVTVPSSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVITLPPS 240

QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
DB 241 LGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVITLPPS 360
DB 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVITLPPS 360

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420
DB 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420

QY 421 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 421 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 2
AAH85199
ID AAY85199 standard; protein; 453 AA.
XX
AC AAY85199;
DT 29-JUN-2000 (first entry)
XX

Heavy chain amino acid sequence of the humanised MaE11 antibody.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FcEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent; chimeric.
XX
OS Mus sp.
OS Homo sapiens.
XX
XX US6037453-A.
XX
XX 14-MAR-2000.
XX
XX 06-JUN-1995; 95US-00466151.
XX
XX 14-AUG-1992; 92WO-US006860.
XX
XX 26-JAN-1994; 94US-00185899.
XX
XX 15-MAR-1995; 95US-00405617.
XX
XX (GETH) GENENTECH INC.
XX
XX Presta LG, Jardieu PM;
XX
XX WPI; 2000-269913/23.
XX
XX New bispecific antibodies, useful for treating immunoglobulin E-mediated
PT disease, binds to IgE, but only when on the low affinity receptor, and to
PT an antigen other than IgE.

Claim 14; Fig 3; 48pp; English.

XX This sequence represents the heavy chain amino acid sequence of a
PS humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention
XX relates to a bispecific antibody that binds specifically to IgE when IgE
CC is bound to its low affinity receptor (FcEL), but does not bind to IgE,
CC when IgE is bound to its high affinity receptor (FcEH). The bispecific
CC antibody comprises an IgE-binding arm with human framework residues of a
CC recipient human antibody and donor murine CDR (complementarity
CC determining region) residues, but with at least one human CDR residue
CC replacing the analogous murine residue. The antibody also comprises an Fv
CC that is specific for a predetermined antigen other than IgE. The
CC antibodies work by displacing bound IgE from its receptor, or via
CC competitive inhibition of its binding. The bispecific antibodies are used
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated
CC diseases, also, when immobilised, for the isolation of FcEL from cells
CC (for research or therapy). The bispecific antibodies of the invention do
CC not cause granulation or release of histamine from mast cells
XX

SQ Sequence 453 AA;

Query Match 100.0%; Score 2432; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.6e-142; Indels 0; Gaps 0;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSINY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSINY 60

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAIVYCARGSHYFGHWHFAVWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDDSKNTFYLMNSLRADTAIVYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180
DB 121 SASTKGKPSVPLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180

QY 181 QSSGLYSLSVTVPSSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVITLPPS 240
DB 181 QSSGLYSLSVTVPSSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPRPQVITLPPS 240

QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
DB 241 LGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVITLPPS 360
DB 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVITLPPS 360

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420
DB 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420

QY 421 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 421 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 3
AAH95659
ID AAW95659 standard; protein; 451 AA.
XX
XX AAW95659;
XX
XX 08-JUN-1999 (first entry)
XX
XX Mus musculus anti-IgE e25 full length variable heavy chain.
XX
XX Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.

XX	Mus musculus.	XX	OS	AAW95661 standard; protein; 451 AA.	XX	OS	AAW95661 standard; protein; 451 AA.
XX	WO9901556-A2.	XX	AC	AAW95661;	XX	AC	AAW95661;
XX	14-JAN-1999.	XX	DT	08-JUN-1999 (first entry)	XX	DT	08-JUN-1999 (first entry)
XX	30-JUN-1998;	XX	DE	Mus musculus anti-IgE e26 full length heavy chain.	XX	DE	Mus musculus anti-IgE e26 full length heavy chain.
XX	02-JUL-1997;	XX	KW	Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;	XX	KW	Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
XX	(GETH) GENENTECH INC.	XX	KW	production; hypersensitivity; allergen; anaphylaxis; atopic allergy;	XX	KW	production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
XX	Lowman HB, Presta LG, Jardieu PM, Lowe J;	XX	KW	asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;	XX	KW	asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
XX	WPI; 1999-106057/09.	XX	KW	anaphylactic shock; urticaria.	XX	KW	anaphylactic shock; urticaria.
XX	Improving affinity of polypeptides, particularly anti-IgE antibodies - by	XX	OS	Mus musculus.	XX	OS	Mus musculus.
XX	identifying aspartyl residues which undergo isomerisation and	XX	PN	WO9901556-A2.	XX	PN	WO9901556-A2.
XX	substituting alternative residues and screening for affinity against the	XX	PD	14-JAN-1999.	XX	PD	14-JAN-1999.
XX	target.	XX	XX	30-JUN-1998;	XX	XX	30-JUN-1998;
XX	Disclosure; Page 92-94; 129pp; English.	XX	PF	02-JUL-1997;	XX	PF	02-JUL-1997;
XX	The sequence is that of the full length heavy chain of e25. It was used as	XX	PR	(GETH) GENENTECH INC.	XX	PR	(GETH) GENENTECH INC.
XX	part of a method to improve the affinity of anti-IgE antibodies such as	XX	XX	Lowman HB, Presta LG, Jardieu PM, Lowe J;	XX	XX	Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX	e26 and e27. The e26 and e27 antibodies can be used for reducing or	XX	XX	WPI; 1999-106057/09.	XX	XX	WPI; 1999-106057/09.
XX	preventing IgE mediated production of histamine in a mammal. They can be	XX	XX	Improving affinity of polypeptides, particularly anti-IgE antibodies - by	XX	XX	Improving affinity of polypeptides, particularly anti-IgE antibodies - by
XX	used for treating a disorder mediated by IgE such as hypersensitivity,	XX	XX	identifying aspartyl residues which undergo isomerisation and	XX	XX	identifying aspartyl residues which undergo isomerisation and
XX	atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,	XX	XX	substituting alternative residues and screening for affinity against the	XX	XX	substituting alternative residues and screening for affinity against the
XX	eczema, anaphylactic shock and urticaria. The antibodies can also be used	XX	XX	target.	XX	XX	target.
XX	for affinity purification, detection and diagnosis	XX	XX	Disclosure; Page 95-96; 129pp; English.	XX	XX	Disclosure; Page 95-96; 129pp; English.
XX	Sequence 451 AA;	XX	XX	The sequence is that of the full length heavy chain of e26. It was used	XX	XX	The sequence is that of the full length heavy chain of e26. It was used
XX	Query Match 98.3%; Score 2391; DB 2; Length 451;	XX	XX	as part of a method to improve the affinity of anti-IgE antibodies such	XX	XX	as part of a method to improve the affinity of anti-IgE antibodies such
XX	Best Local Similarity 98.9%; Pred. No. 2.2e-139;	XX	XX	e26 and e27. The e26 and e27 antibodies can be used for reducing or	XX	XX	e26 and e27. The e26 and e27 antibodies can be used for reducing or
XX	Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;	XX	XX	preventing IgE mediated production of histamine in a mammal. They can be	XX	XX	preventing IgE mediated production of histamine in a mammal. They can be
QY	1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60	QY	1	EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60	QY	1	EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60
DB	1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60	DB	1	EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60	DB	1	EVQLVESGGGLVQPGGSLRLSCAVSGYISITGYSNWNIRQAPGKLEWVASITYDGSNTY 60
QY	61 ADSVKGRFTISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120	QY	61	ADSVKGRFTISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120	QY	61	ADSVKGRFTISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120
DB	61 NFSVKGRITISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120	DB	61	NFSVKGRITISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120	DB	61	NFSVKGRITISRDDSKNTFYLQMSRLRAEDTAVVYCARGSHYFGHHFPAVWGQGLTVTS 120
QY	121 SASTKGKPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 180	QY	121	SASTKGKPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 180	QY	121	SASTKGKPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 180
DB	121 SAST--KGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178	DB	121	SAST--KGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178	DB	121	SAST--KGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
QY	181 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 240	QY	181	QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 240	QY	181	QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 240
DB	179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 238	DB	179	QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 238	DB	179	QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPPCPAPEL 238
QY	241 LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 300	QY	241	LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 300	QY	241	LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 300
DB	239 LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 298	DB	239	LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 298	DB	239	LGGPSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNATKPREE 298
QY	301 QYNSTYRVSVLTFLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPS 360	QY	301	QYNSTYRVSVLTFLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQRPFPQVYTLPPS 360	QY	301	QYNSTYRVSVLTFLVHODWLNKGEYKCKVSNKALPAPIEKTISKAK

RESULT 4

Db 299 QNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 5
ID AAY85201
XX AAY85201 standard; protein; 451 AA.
AC AAY85201;
XX
DT 29-JUN-2000 (first entry)
XX
DE Light chain amino acid sequence of anti-human IgE antibody.
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent.
XX
OS Mus sp.
XX
US 6037453-A.
PN
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-00466151.
XX
PR 14-AUG-1992; 92WO-US006860.
PR 26-JAN-1994; 94US-00185899.
PR 15-MAR-1995; 95US-00405617.
XX
PA (GETH) GENENTECH INC.
XX
XX Presta LG, Jardieu PM;
PI
XX WPI; 2000-269913/23.
DR
XX
PT New bispecific antibodies, useful for treating immunoglobulin E-mediated
PT disease, binds to IgE, but only when on the low affinity receptor, and to
PT an antigen other than IgE.
XX
XX Claim 15; Col 73-76; 48pp; English.
PS
XX
CC This sequence represents the light chain amino acid sequence of a mouse
CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a
CC bispecific antibody that binds specifically to IgE when IgE is bound to
CC its low affinity receptor (FCEL), but does not bind to IgE, when IgE is
CC bound to its high affinity receptor (FCEH). The bispecific antibody
CC comprises an IgE-binding arm with human framework residues of a recipient
CC human antibody and donor murine CDR (complementarity determining region)
CC residues, but with at least one human CDR residue replacing the analogous
CC murine residue. The antibody also comprises an Fv that is specific for a
CC predetermined antigen other than IgE. The antibodies work by displacing
CC bound IgE from its receptor, or via competitive inhibition of its
CC binding. The bispecific antibodies are used for diagnosis, treatment and
CC prevention of allergy and other IgE-mediated diseases, also, when
CC immobilised, for the isolation of FCEL from cells (for research or
CC therapy). The bispecific antibodies of the invention do not cause
CC granulation or release of histamine from mast cells
XX
SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. NO. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAVSYSITSGYSNNWIRQAPKGLWVASITYDGSTNY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAVSYSITSGYSNNWIRQAPKGLWVASITYDGSTNY 60
QY 61 ADSVKGRTISRDDSKNTFYLQWNSLRADETAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQWNSLRADETAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKCKGPSVFPLDPPSSKSTSGGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLDPPSSKSTSGGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPEL 240
Db 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPCPAPEL 238
QY 241 LGGPSVFLPFPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPFPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 6
AAB47088
ID AAB47088 standard; protein; 451 AA.
XX
AC AAB47088;
XX
DT 11-SEP-2003 (revised)
DT 08-MAY-2001 (first entry)
XX
XX Anti-IgE antibody, E26, heavy chain.
XX
KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;
KW green fluorescent protein; GFP; promoter; expression.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
XX WO200104306-A1.
XX
PD 18-JAN-2001.
XX
PF 11-JUL-2000; 2000WO-US018841.
XX
PR 12-JUL-1999; 99US-0143360P.
XX
XX (GETH) GENENTECH INC.
XX
XX Chisholm V, Crowley CW, Krummen LA, Meng YG;
XX WPI; 2001-138352/14.
XX
PT Novel polynucleotide construct for screening and obtaining cells
PT expressing high levels of desired protein, comprises amplifiable
PT selectable gene, fluorescent protein gene and sequence encoding desired
PT product.
XX
XX Disclosure; Fig 13B; 75pp; English.
XX
XX The sequences given in AAB47087-88 represent the light and heavy chains
CC

CC of the anti-IgE antibody, E26. These sequences were expressed by the
CC construct of the invention, which comprises an amplifiable selectable
CC gene, a green fluorescent protein gene (GFP), and a selected sequence
CC encoding a desired product, which is operably linked to either the
CC amplifiable selectable gene or to the GFP gene, and to a promoter.
CC Constructs such as this, are useful for producing a desired product by
CC introduction into a suitable eukaryotic cell, culturing the resultant
CC eukaryotic cell under conditions so as to express the desired product,
CC and recovering the desired product from the culture medium. The
CC constructs are efficient for identifying and selecting for stable
CC eukaryotic cells expressing high levels of a desired product. They are
CC suitable for earlier and faster screening of transfected cells. (Updated
CC on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSINY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSINY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQNSLRRAEDTAVYICARGSHYFGHHFPAWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRRAEDTAVYICARGSHYFGHHFPAWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGTAAALGCLVKDYRPEPTVYVSNWNGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVKDYRPEPTVYVSNWNGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKTKPREE 300
DB 239 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 7
AAB76948
ID AAB76948 standard; protein; 451 AA.
AC AAB76948;
XX
XX 17-APR-2001 (first entry)
DE Full length heavy chain sequence of e25 SEQ ID 14.
XX
XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
XX Synthetic.
XX
XX US6172213-B1.
XX
XX 09-JAN-2001.
XX

PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
XX WPI; 2001-122353/13.

XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
XX

PS Disclosure; Fig 12; 87pp; English.

XX This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules, and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IGE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX

SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSINY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSINY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQNSLRRAEDTAVYICARGSHYFGHHFPAWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRRAEDTAVYICARGSHYFGHHFPAWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGTAAALGCLVKDYRPEPTVYVSNWNGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVKDYRPEPTVYVSNWNGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKTKPREE 300
DB 239 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

Db 121 SAST--KGFSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNKHPSNTKVDKKVEPKSCDKTHTCTPCPAPAPL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNKHPSNTKVDKKVEPKSCDKTHTCTPCPAPAPL 238
QY 241 LGGFSVFLFPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPRE 300
Db 239 LGGFSVFLFPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPRE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFPSCSVWHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFPSCSVWHEALHNHYTQKSLSLSPGK 451
RESULT 9
AAW95663
ID AAW95663 standard; protein; 451 AA.
XX
AC AAW95663;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e27 full length heavy chain.
XX
KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PP 30-JUN-1998; 98WO-US013410.
XX
PR 02-JUL-1997; 97US-00887352.
XX (GETH) GENENTECH INC.
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX WPI; 1999-106057/09.
XX
PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
PS Disclosure; Page 97-99; 129pp; English.
XX
CC The sequence is that of the full length heavy chain of e27. It was used
CC as part of a method to improve the affinity of anti-IgE antibodies such
CC as e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IgE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis
XX
SQ Sequence 451 AA;

RESULT 8
AAB76950
ID AAB76950 standard; protein; 451 AA.
XX
AC AAB76950;
XX
DT 17-APR-2001 (first entry)
XX
DE Full length heavy chain sequence of e26 SEQ ID 16.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX (GETH) GENENTECH INC.
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX WPI; 2001-122353/13.
XX
PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
PS Claim 2; Fig 12; 87pp; English.
XX
CC This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules, and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
SQ Sequence 451 AA;
Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 449; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVOLVSGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPKGLWVASITDGSTNY 60
Db 1 EVOLVSGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPKGLWVASITDGSTNY 60
QY 61 ADSVKGRFTISRDSKNTFFLQNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDSKNTFFLQNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTYKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180

Query Match 97.4%; Score 2369; DB 2; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

QY 61 ADSVKGRTTISRDDSKNTFYLMNSLRADTAIVYCARSHYFGHWHFAVWGQGLTVTVS 120
DB 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYCARSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPPEPVTVSNWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTGGTAALGCLVKDYFPPEPVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 240
DB 179 QSSGLYSLSVSVTVSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 10
AAV50031
ID AAV50031 standard; protein; 451 AA.
XX
AC AAV50031;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human E27 anti-IgE antibody heavy chain.
XX
KW Immunoglobulin E; IgE; antibody; vascular endothelial growth factor;
KW VEGF; chimeric; IgG; assay; Fc gamma receptor; low affinity; hexamer;
KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
XX heavy chain.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9951642-A1.
XX
XX 14-OCT-1999.
XX
XX 31-MAR-1999; 99WO-US006858.
XX
XX 02-APR-1998; 98US-00054255.
XX
XX 15-JAN-1999; 99US-0116100P.
XX
XX (GETH) GENENTECH INC.
XX
XX Idusogie EE, Mulkerrin MG, Presta LG, Shields RL;
XX
XX WPI; 1999-620197/53.
XX
XX Antibody variants useful in receptor binding assays and in therapy of
XX conditions needing treatment.
XX

Example 1; Fig 4B; 69pp; English.

This sequence represents human E27 anti-IgE (immunoglobulin E) antibody heavy chain, which, along with the E27 light chain (AAV50030), comprises the E27 anti-IgE antibody. The E27 antibody binds the constant regions of IgE, and when mixed with IgE in an equimolar ratio, forms a stable hexamer consisting of three E27 molecules and 3 IgE molecules. This complex-forming ability can be utilised in an assay for the binding of IgG to Fc gamma receptors Fc-gamma-1a, Fc-gamma-1b and Fc-gamma-1c, which have IgG affinities in the micromolar range and so cannot be assayed via a standard ELISA (enzyme-linked immunosorbent assay) protocol. The low affinity receptor binding assay uses E27 and a recombinant chimeric form of IgE, consisting of a human IgE Fc region and the Fab regions of an anti-VEGF (vascular endothelial growth factor) antibody, which binds two VEGF molecules per mole of anti-VEGF chimeric IgE. When recombinant human VEGF is added at 2:1 molar ratio to the IgE:E27 hexamer complexes, the hexamers are linked into larger complexes via IgE Fab-VEGF interactions. The E27 component of this complex binds to the Fc-gamma-1a, Fc-gamma-1b and Fc-gamma-1c alpha subunits to permit detection via ELISA

XX
SQ Sequence 451 AA;

Query Match 97.4%; Score 2369; DB 2; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVOLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

QY 61 ADSVKGRTTISRDDSKNTFYLMNSLRADTAIVYCARSHYFGHWHFAVWGQGLTVTVS 120
DB 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAIVYCARSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPPEPVTVSNWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTGGTAALGCLVKDYFPPEPVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSVSVTVSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVSVTVSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPCPAPEL 238

QY 241 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
AAB07473
ID AAB07473 standard; protein; 451 AA.
XX
AC AAB07473;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of E27 and anti-IgE antibody heavy chain.
XX
XX anti-IgE antibody; heavy chain; Fc region; effector function; cancer;
XX allergy; asthma; LfA-1-mediated disorder; tumour; cancer.
XX

OS Synthetic.
XX WO200042072-A2.
XX 20-JUL-2000.
XX 14-JAN-2000; 2000WO-US000973.
XX 15-JAN-1999; 99US-0116023P.
XX (GETH) GENENTECH INC.
XX Presta LG;
XX WPI; 2000-476035/41.
XX New Fc region-containing polypeptides that have altered effector function
PT due to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX
XX Disclosure; Fig 4B; 132pp; English.
XX
XX The present sequence represents the E27 and anti-IgE antibody heavy
CC chain. The protein is used to produce Fc region-containing polypeptides
CC that have altered effector function as a consequence of one or more amino
CC acid modifications in the Fc region. The variant polypeptides are useful
CC for treating cancer, allergic conditions such as asthma (with an anti-IgE
CC antibody), and LFA-1-mediated disorders. Where the polypeptide binds the
CC HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a
CC benign or malignant tumour characterized by overexpression of the HER2
CC receptor. Such cancers include breast cancer, squamous cell cancer, small
CC -cell lung cancer, non-small cell lung cancer, gastrointestinal cancer,
CC pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder
CC cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma,
CC salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer,
CC vulval cancer, thyroid cancer, hepatic carcinoma and various types of
CC head and neck cancer
XX
XX Sequence 451 AA;
SQ

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWASITYDGSNTY 60
DB 1 EVLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWASIKYSGETKY 60
QY 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAVYVCARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAVYVCARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKGKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVSGALTSVHTFPAVL 180
DB 121 SAST--KGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVSGALTSVHTFPAVL 178
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTPKVKPEKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTPKVKPEKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
DB 239 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVLDHQLNKEPKYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLDHQLNKEPKYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYSLKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYSLKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453

DB 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 451
RESULT 12
AAB76952
ID AAB76952 standard; protein; 451 AA.
XX AAB76952;
AC AAB76952;
DT 17-APR-2001 (first entry)
XX Full length heavy chain sequence of e27 SEQ ID 18.
DE
XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
OS Synthetic.
XX
XX US6172213-B1.
PN
XX 09-JAN-2001.
PD
XX 30-JUN-1998; 98US-00109207.
PF
XX 02-JUL-1997; 97US-0051554P.
PR
XX (GETH) GENENTECH INC.
PA
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI WPI; 2001-122353/13.
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
XX Claim 4; Fig 12; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules, and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
XX Sequence 451 AA;
SQ

Query Match 97.4%; Score 2369; DB 4; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWASITYDGSNTY 60
DB 1 EVLVESGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWASIKYSGETKY 60
QY 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAVYVCARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLMNSLRADTAVYVCARGSHYFGHWHFAVWGQGLTVTS 120

XX The invention relates to a new isolated nucleic acid that encodes an
CC antibody variant that binds antigen or an immunoadhesin variant that
CC binds a ligand or receptor. The antibody or immunoadhesin variant
CC comprises a human immunoglobulin G Fc region. The nucleic acid is useful
CC for preparing a composition for treating a disorder e.g. autoimmune
CC disorder. The present sequence represents the amino acid sequence of the
CC E27 anti-immunoglobulin E antibody heavy chain
XX
SQ Sequence 451 AA;

Query Match 97.4%; Score 2369; DB 6; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-136;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLCAVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLCAVSGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60

QY 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NFSVKGRTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120

QY 121 SASTKKGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 180
Db 121 SAST--KGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 178

QY 181 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPEL 240
Db 179 QSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPEL 238

QY 241 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
Db 239 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298

QY 301 QYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
AAY29458
ID AAY29458 standard; protein; 452 AA.
XX
AC AAY29458;
XX
DT 05-OCT-1999 (first entry)
XX
DE Recombinant immunoglobulin SEQ ID NO:71.
XX
KW Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KW fusion protein.
XX
OS Synthetic.
XX
DN WO993779-A1.
XX
PD 29-JUL-1999.
XX
PF 19-JAN-1999; 99WO-US001081.
XX
PR 22-JAN-1998; 98US-00012116.
PR 20-FEB-1998; 98WO-US003337.
PR 24-JUL-1998; 98US-00121952.

PR 24-JUL-1998; 98US-00122513.
XX (GETH) GENENTECH INC.
XX
XX Hsai V, Koumenis I, Leong SJ, Presta LG, Shahrokhi Z, Zapata GA;
XX WPI; 1999-469134/39.
XX
XX New conjugates of nonproteinaceous polymers with antibody fragments, used
PT for treating inflammatory disorders.
XX
XX Disclosure; Page 354-355; 360pp; English.
XX
XX The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic
CC reperfusion disorder, and autoimmune diseases. They can also be used for
CC treating e.g. inflammatory skin diseases including psoriasis and atopic
CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
CC The conjugates can also be used as reagents in an animal model system for
CC in vivo study of the biological functions of the antigen recognised by
CC the conjugate. The present sequence represents a recombinant
CC immunoglobulin protein from the present invention
XX
SQ Sequence 452 AA;

Query Match 91.1%; Score 2214.5; DB 2; Length 452;
Best Local Similarity 92.7%; Pred. No. 1.7e-128;
Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLCAVSGYSITSGYSNNWIRQAPGKLEWVASI-TYDGSNT 59
Db 1 EVQLVESGGGLVQPGGSLRLCAVSGYSITSGYSNNWIRQAPGKLEWVYIDPSNGETT 59

QY 60 YADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSH-YFGHWHFAVWGQGLTVT 118
Db 60 YNOKFGKFTLSDNSKNTAYLOMNSLRADTAIVYICARGDYRYNGDWFDFVWGQGLTVT 119

QY 119 VSSASTKKGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 178
Db 120 VSSAST--KGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 177

QY 179 VLQSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 238
Db 178 VLQSSGLYSLSVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAP 237

QY 239 ELGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 238 ELGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 297

QY 299 EEQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 358
Db 298 EEQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 357

QY 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 418
Db 358 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 417

QY 419 DKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 418 DKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 452

Search completed: May 13, 2004, 15:45:25
Job time : 71.1863 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:38 ; Search time 22.2787 Seconds
(without alignments)
1049.728 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHHYTKSLSPK 453

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMS.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMS.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMS.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMS.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMS.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	453	US-08-466-151-8	Sequence 8, Appli
2	2432	100.0	453	US-08-466-151-8	Sequence 8, Appli
3	2432	100.0	453	US-08-466-151-8	Sequence 8, Appli
4	2391	98.3	451	US-08-887-352B-14	Sequence 14, Appl
5	2391	98.3	451	US-08-887-352B-16	Sequence 16, Appl
6	2391	98.3	451	US-08-466-151-65	Sequence 65, Appl
7	2391	98.3	451	US-09-109-207C-14	Sequence 14, Appl
8	2391	98.3	451	US-09-109-207C-16	Sequence 16, Appl
9	2391	98.3	451	US-09-286-005-14	Sequence 14, Appl
10	2391	98.3	451	US-09-286-005-16	Sequence 16, Appl
11	2391	98.3	451	US-09-920-171-14	Sequence 14, Appl
12	2391	98.3	451	US-09-920-171-16	Sequence 16, Appl
13	2369	97.4	451	US-08-887-352B-18	Sequence 18, Appl
14	2369	97.4	451	US-09-109-207C-18	Sequence 18, Appl
15	2369	97.4	451	US-09-282-505-2	Sequence 2, Appli
16	2369	97.4	451	US-09-054-255-2	Sequence 2, Appli
17	2369	97.4	451	US-08-286-005-18	Sequence 18, Appl
18	2369	97.4	451	US-08-286-005-16	Sequence 16, Appl
19	2369	97.4	451	US-09-680-145-2	Sequence 2, Appli
20	2369	97.4	451	US-09-920-171-18	Sequence 18, Appl
21	2214.5	91.1	452	US-09-027-449-71	Sequence 71, Appl
22	2214.5	91.1	452	US-09-026-985-71	Sequence 71, Appl
23	2214.5	91.1	452	US-09-131-952A-71	Sequence 71, Appl
24	2214.5	91.1	452	US-09-234-340A-71	Sequence 71, Appl
25	2179.5	89.6	449	US-09-679-397-2	Sequence 2, Appli
26	2179.5	89.6	449	US-09-680-148-2	Sequence 2, Appli
27	2179.5	89.6	449	US-09-304-465A-2	Sequence 2, Appli

Sequence 7, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 7, Appli
Sequence 67, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 90, Appli
Sequence 8, Appli
Sequence 27, Appli
Sequence 81, Appli
Sequence 70, Appli
Sequence 4, Appli

28 2164.5 89.0 459 1 US-08-157-101A-7
29 2132 87.7 478 3 US-08-487-550-8
30 2132 87.7 478 4 US-09-526-098-8
31 2117.5 87.1 473 3 US-09-049-672A-4
32 2093 86.1 476 3 US-08-487-550-12
33 2093 86.1 476 4 US-09-526-098-12
34 2092 86.0 449 1 US-08-458-516-13
35 2078 85.4 472 4 US-08-793-450-8
36 2073.5 85.3 446 3 US-08-397-411-7
37 2069 85.1 468 4 US-09-485-737B-67
38 2069 85.1 476 3 US-08-487-550-4
39 2069 85.1 476 4 US-09-526-098-4
40 2069 85.1 711 4 US-09-485-737B-90
41 2056.5 84.6 457 3 US-09-049-672A-8
42 2056.5 84.6 475 4 US-09-740-002-27
43 2052.5 84.4 467 1 US-08-704-744-81
44 2050 84.3 451 4 US-09-472-087-70
45 2047 84.2 443 5 PCT-US96-13152-4

ALIGNMENTS

RESULT 1
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid

TOPOLOGY: Linear
US-08-466-151-8

Query Match 100.0%; Score 2432; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKKGKSVPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSNWNSGALTSGVHTFPAVL 180
DB 121 SASTKKGKSVPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSNWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 240
DB 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 240
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 301 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
DB 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 2

US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-08-466-163B-8

Query Match 100.0%; Score 2432; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60

DB 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKKGKSVPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSNWNSGALTSGVHTFPAVL 180
DB 121 SASTKKGKSVPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSNWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 240
DB 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 240
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 301 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
DB 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 3

US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-802-096-8

Query Match 100.0%; Score 2432; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
DB 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKKGKPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVL 180
 Db 121 SASTKKGKPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVL 180
 QY 181 QSSGLYSLSSVTVVPSSSLSGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPEL 240
 Db 181 QSSGLYSLSSVTVVPSSSLSGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPEL 240
 QY 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
 Db 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
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 Db 301 QYNSTRYVSVLTVLHODWLNKGEVKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
 QY 361 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDK 420
 Db 361 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDK 420
 QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
 Db 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 4

US-08-887-352B-14
 ; Sequence 14, Application US/08887352B
 ; Patent No. 5994511
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 ; TITLE OF INVENTION: Improving Polypeptides
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,352B
 ; FILING DATE: 03-Jul-1997
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P1123
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-887-352B-14

Query Match 98.3%; Score 2391; DB 2; Length 451;
 Best Local Similarity 98.9%; Pred. No. 3.6e-181;
 Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPKGLEWVASITYDGSTNY 60
 Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPKGLEWVASITYDGSTNY 60

QY 61 ADSVGRFTISRDDSKNTFYLQNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
 Db 61 NPSVKGRITISRDDSKNTFYLQNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
 QY 121 SASTKKGKPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVL 180
 Db 121 SASTKKGKPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVL 178
 QY 181 QSSGLYSLSSVTVVPSSSLSGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPEL 240
 Db 179 QSSGLYSLSSVTVVPSSSLSGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPEL 238
 QY 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
 Db 239 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
 QY 301 QYNSTRYVSVLTVLHODWLNKGEVKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
 Db 299 QYNSTRYVSVLTVLHODWLNKGEVKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
 QY 361 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDK 420
 Db 359 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDK 418
 QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
 Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 5

US-08-887-352B-16
 ; Sequence 16, Application US/08887352B
 ; Patent No. 5994511
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 ; TITLE OF INVENTION: Improving Polypeptides
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,352B
 ; FILING DATE: 03-Jul-1997
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P1123
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-887-352B-16

Query Match 98.3%; Score 2391; DB 2; Length 451;
 Best Local Similarity 98.9%; Pred. No. 3.6e-181;
 Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPKGLEWVASITYDGSTNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRAPGKGLWEVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRADDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NPSVKGRFTISRDDSKNTFYQMNSLRADDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSTSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVVTVPSSTSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 6
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65
Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181; Indels 2; Gaps 1;
Matches 448; Conservative 0; Mismatches 3;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRAPGKGLWEVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRAPGKGLWEVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRADDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
Db 61 NPSVKGRFTISRDDSKNTFYQMNSLRADDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSTSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVVTVPSSTSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 7
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptid
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14
Query Match 98.3%; Score 2391; DB 3; Length 451;

Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 ADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120

Qy 121 SASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

Qy 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

Qy 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 358

Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418

Qy 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAB11
US-09-109-207C-16

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 ADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120

Qy 121 SASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

Qy 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

Qy 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 358

Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

Qy 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 358

Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418

Qy 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAB11
US-09-296-005-14

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 ADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120

Qy 121 SASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

Qy 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

Qy 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 451

RESULT 10
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; PRIOR FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTS 120
Db 61 NPSVKGRTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTS 120
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFPLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVVEVHNAKTKPREE 300
Db 239 LGGPSVFPLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVHLQDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVHLQDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 451

RESULT 11
US-09-920-171-14
; Sequence 14, Application US/09920171

; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASITVDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTS 120
Db 61 NPSVKGRTISRDDSKNTFYLQMSLRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTS 120
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFPLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVVEVHNAKTKPREE 300
Db 239 LGGPSVFPLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVHLQDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVHLQDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 451

RESULT 12
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-18; Indels 2; Gaps 1;
Matches 448; Conservative 0; Mismatches 3;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGGQGGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGGQGGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRRAEDTAVYYCARGSHYFGHWHPAVWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQMSLRRAEDTAVYYCARGSHYFGHWHPAVWGQGLTVTS 120
QY 121 SASTKKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNNAKTKPREE 300
DB 239 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFPLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 13
US-08-887-352B-18
Sequence 18, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B

FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-18

Query Match 97.4%; Score 2369; DB 2; Length 451;
Best Local Similarity 98.0%; Pred. No. 2e-179; Indels 2; Gaps 1;
Matches 444; Conservative 0; Mismatches 7;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGGQGGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGGQGGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRRAEDTAVYYCARGSHYFGHWHPAVWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQMSLRRAEDTAVYYCARGSHYFGHWHPAVWGQGLTVTS 120
QY 121 SASTKKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVVTVPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNNAKTKPREE 300
DB 239 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFPLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFPLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 14
US-09-109-207C-18
Sequence 18, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,207C

OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-18

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTVS 120
DB 61 NPSVKGRITISRDDSKNTFYIQMNSLRRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGVFSCSVMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 15

US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTVS 120
DB 61 NPSVKGRITISRDDSKNTFYIQMNSLRRAEDTAVYICARGSHYFGHWHPAVWGQGLTVTVS 120

QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 240
DB 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREE 300
DB 239 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
DB 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGVFSCSVMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQQGVFSCSVMEALHNHYTQKSLSLSPGK 451

Search completed: May 13, 2004, 15:48:47
Job time : 23.2787 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:47:29 ; Search time 52.6587 Seconds
(without alignments)
2393.762 Million cell updates/sec

Title: US-09-925-179-8

Perfect score: 2432

Sequence: 1 EVQLVESGGGLVQPGSLRL.....MHEALHNYTKSLSPCK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	453	9	US-09-802-077-8
2	2432	100.0	453	9	US-09-802-096-8
3	2432	100.0	453	10	US-09-925-179-8
4	2391	98.3	451	9	US-09-920-171-14
5	2391	98.3	451	9	US-09-920-171-16
6	2391	98.3	451	10	US-09-925-179-65
7	2391	98.3	451	14	US-10-113-996-14
8	2391	98.3	451	14	US-10-113-996-16
9	2388	98.2	451	10	US-09-925-179-66
10	2379	97.8	451	10	US-09-925-179-68
11	2369	97.4	451	9	US-09-920-171-18
12	2369	97.4	451	10	US-09-792-938-2
13	2369	97.4	451	14	US-10-113-996-18
14	2369	97.4	451	14	US-10-292-869-2
15	2214.5	91.1	452	10	US-09-726-258-71

16	2210	90.9	475	14	US-10-020-785-11	Sequence 11, Appl
17	2207.5	90.8	447	16	US-10-474-832-4	Sequence 4, Appl
18	2204.5	90.6	477	15	US-10-291-265-395	Sequence 395, Appl
19	2204	90.6	451	15	US-10-423-293-4	Sequence 4, Appl
20	2202.5	90.6	445	14	US-10-320-231A-79	Sequence 79, Appl
21	2201.5	90.5	447	16	US-10-474-832-5	Sequence 5, Appl
22	2197.5	90.4	447	16	US-10-474-832-6	Sequence 6, Appl
23	2182	89.7	445	16	US-10-408-901-42	Sequence 42, Appl
24	2182	89.7	449	9	US-09-736-371B-21	Sequence 21, Appl
25	2182	89.7	449	15	US-10-463-442-21	Sequence 10, Appl
26	2181.5	89.6	449	14	US-10-253-366-2	Sequence 2, Appl
27	2179.5	89.6	449	14	US-10-316-694-2	Sequence 2, Appl
28	2179.5	89.6	449	14	US-10-356-974-2	Sequence 2, Appl
29	2179.5	89.6	449	15	US-10-423-299-2	Sequence 2, Appl
30	2179.5	89.6	449	16	US-10-659-825-2	Sequence 3, Appl
31	2179.5	89.6	449	16	US-09-848-832-3	Sequence 3, Appl
32	2178	89.6	474	10	US-10-225-108A-3	Sequence 1, Appl
33	2178	89.6	474	14	US-10-461-148-1	Sequence 6, Appl
34	2177.5	89.5	444	14	US-10-150-475A-6	Sequence 12, Appl
35	2177	89.5	451	9	US-09-822-698A-26	Sequence 38, Appl
36	2176.5	89.5	442	12	US-10-226-435A-12	Sequence 16, Appl
37	2176.5	89.5	446	16	US-10-408-901-38	Sequence 16, Appl
38	2175.5	89.5	479	15	US-10-418-836-16	Sequence 4681, Ap
39	2175.5	89.3	473	15	US-10-108-260A-4681	Sequence 32, Appl
40	2172.5	89.2	663	12	US-10-412-406-32	Sequence 33, Appl
41	2170.5	89.2	4852	12	US-10-412-406-33	Sequence 46, Appl
42	2170.5	89.2	4852	12	US-10-108-260A-4640	Sequence 46, Appl
43	2168	89.1	474	15	US-10-408-901-46	Sequence 26, Appl
44	2167.5	89.1	446	16	US-10-029-926B-26	
45	2161	88.9	464	12		

ALIGNMENTS

RESULT 1

US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

Query Match 100.0%; Score 2432; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGSLRLSCAVSGYSITSGYNNIRQAPGKLEWVASITVDGSTNY 60

Db 1 EVQLVESGGGLVQPGSLRLSCAVSGYSITSGYNNIRQAPGKLEWVASITVDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180
DB 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
DB 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
QY 241 LGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVTLVHLDWLNKGEYKCKVSNKALPAIEKTIKAKGQPREPQVYTLPPS 360
DB 301 QYNSTYRVVSVTLVHLDWLNKGEYKCKVSNKALPAIEKTIKAKGQPREPQVYTLPPS 360
QY 361 REEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
DB 361 REEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPOK 453
DB 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPOK 453

RESULT 2

US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-802-096-8

Query Match 100.0%; Score 2432; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSTNY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180

DB 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
DB 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240
QY 241 LGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
DB 241 LGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVTLVHLDWLNKGEYKCKVSNKALPAIEKTIKAKGQPREPQVYTLPPS 360
DB 301 QYNSTYRVVSVTLVHLDWLNKGEYKCKVSNKALPAIEKTIKAKGQPREPQVYTLPPS 360
QY 361 REEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
DB 361 REEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPOK 453
DB 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPOK 453

RESULT 3

US-09-925-179-8
; Sequence 8, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-925-179-8

Query Match 100.0%; Score 2432; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSTNY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 ADSVKGRFTISRDDSKNTFYLOMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180
DB 121 SASTKKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSNWSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSVVTVFSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPEL 240

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Db 181 QSSGLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Qy 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Qy 301 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 301 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Qy 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453
Db 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453

RESULT 4
US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMWIRQAPGKGLEWVASITYDGSNTY 60
Qy 61 ADSVKGRFTISRDDSKNTFYLQVNSLRAREDYAVYCARGSHYFGHHFAVMGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQVNSLRAREDYAVYCARGSHYFGHHFAVMGQGLTVTVS 120
Qy 121 SASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPEL 238
Qy 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Qy 301 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 298
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 299 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

RESULT 5
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMWIRQAPGKGLEWVASITYDGSNTY 60
Qy 61 ADSVKGRFTISRDDSKNTFYLQVNSLRAREDYAVYCARGSHYFGHHFAVMGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQVNSLRAREDYAVYCARGSHYFGHHFAVMGQGLTVTVS 120
Qy 121 SASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPEL 238
Qy 241 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Qy 301 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

RESULT 6
```

US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P07182C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tabl
US-09-925-179-65

Query Match 98.3%; Score 2391; DB 10; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVOLVESGGLVQPGSLRLSCAVSGYITSGYSNNWIRQAPGKLEWASITVDGSTNY 60
Db 1 EVOLVESGGLVQPGSLRLSCAVSGYITSGYSNNWIRQAPGKLEWASITVDGSTNY 60

QY 61 ADSVKGRTISRDDSKNTFYLMNSLRABDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120
Db 61 NFSVKGRTISRDDSKNTFYLMNSLRABDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120

QY 121 SASTKKGSPVPLAPSSKSTSGGTAALGCLVKDYFPPSVTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGSPVPLAPSSKSTSGGTAALGCLVKDYFPPSVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 7
US-10-113-996-14
; Sequence 14, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:

; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-14

Query Match 98.3%; Score 2391; DB 14; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVOLVESGGLVQPGSLRLSCAVSGYITSGYSNNWIRQAPGKLEWASITVDGSTNY 60
Db 1 EVOLVESGGLVQPGSLRLSCAVSGYITSGYSNNWIRQAPGKLEWASITVDGSTNY 60

QY 61 ADSVKGRTISRDDSKNTFYLMNSLRABDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120
Db 61 NFSVKGRTISRDDSKNTFYLMNSLRABDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120

QY 121 SASTKKGSPVPLAPSSKSTSGGTAALGCLVKDYFPPSVTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGSPVPLAPSSKSTSGGTAALGCLVKDYFPPSVTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKKOTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-10-113-996-16
; Sequence 16, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-16

Query Match 98.3%; Score 2391; DB 14; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIWIRQAPGKGLWVASITYDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIWIRQAPGKGLWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRAEDTAVVYCARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVVYCARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREE 300
DB 239 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREE 298
QY 301 QYNSTYRVSVLTVLHQQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVSVLTVLHQQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSKLTVDK 418
QY 421 SRWQGNVFSCVWMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFSCVWMEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of Tab
US-09-925-179-66

Query Match 98.2%; Score 2388; DB 10; Length 451;
Best Local Similarity 98.7%; Pred. No. 1.2e-156;
Matches 447; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIWIRQAPGKGLWVASITYDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIWIRQAPGKGLWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRAEDTAVVYCARGSHYFGHWHFAVWGQGLTVTS 120
DB 61 NPSLKGRIITISRDDSKNTFYQMNSLRAEDTAVVYCARGSHYFGHWHFAVWGQGLTVTS 120
QY 121 SASTKKGPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPEL 240
DB 179 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVPEKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREE 300
DB 239 LGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREE 298
QY 301 QYNSTYRVSVLTVLHQQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 360
DB 299 QYNSTYRVSVLTVLHQQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSKLTVDK 418
QY 421 SRWQGNVFSCVWMEALHNHYTQKSLSLSPGK 453
DB 419 SRWQGNVFSCVWMEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68

; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
 US-09-925-179-68

Query Match 97.8%; Score 2379; DB 10; Length 451;
 Best Local Similarity 97.8%; Pred. No. 4.9e-156;
 Matches 443; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
DB	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
QY	61	ADSVKGRFTISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
DB	61	NPSVKGRITISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
QY	121	SASTKGKPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	180
DB	121	SAST--KGPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	178
QY	181	QSSGLYSLSV	VTVPSSSLG	TQTYICNVN	HKPSNTKVDK	KVEPKSCDK	240
DB	179	QSSGLYSLSV	VTVPSSSLG	TQTYICNVN	HKPSNTKVDK	KVEPKSCDK	238
QY	241	LGSPSVFLP	PPPKPOTL	MSRTPEVTC	VVDVSH	EDPEVKFNWYD	300
DB	239	LGSPSVFLP	PPPKPOTL	MSRTPEVTC	VVDVSH	EDPEVKFNWYD	298
QY	301	QYNSTYRV	SVSLTVLH	QDWLNK	KEYCKV	SNKALPAPI	360
DB	299	QYNSTYRV	SVSLTVLH	QDWLNK	KEYCKV	SNKALPAPI	358
QY	361	REMTKNQV	SLTCLV	KGFYPSD	IAVWESNG	OPENNYKTP	420
DB	359	REMTKNQV	SLTCLV	KGFYPSD	IAVWESNG	OPENNYKTP	418
QY	421	SRWQGNV	FSCSVW	HEALHNH	YTKSLS	SPGK	453
DB	419	SRWQGNV	FSCSVW	HEALHNH	YTKSLS	SPGK	451

RESULT 11
 US-09-920-171-18
 ; Sequence 18, Application US/0920171
 ; Patent No. US20020054878A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lowman, Henry B.
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Lowe, John
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
 ; FILE REFERENCE: P1123C2US
 ; CURRENT APPLICATION NUMBER: US/09/920,171
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: US 08/887,352
 ; PRIOR FILING DATE: 1997-07-02
 ; PRIOR APPLICATION NUMBER: US 09/296,005
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 18
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Heavy chain sequence derived from MAb11
 US-09-920-171-18

Query Match 97.4%; Score 2369; DB 9; Length 451;
 Best Local Similarity 98.0%; Pred. No. 2.4e-155;
 Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
DB	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
QY	61	ADSVKGRFTISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
DB	61	NPSVKGRITISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
QY	121	SASTKGKPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	180
DB	121	SAST--KGPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	178
QY	181	QSSGLYSLSV	VTVPSSSLG	TQTYICNVN	HKPSNTKVDK	KVEPKSCDK	240
DB	179	QSSGLYSLSV	VTVPSSSLG	TQTYICNVN	HKPSNTKVDK	KVEPKSCDK	238
QY	241	LGSPSVFLP	PPPKPOTL	MSRTPEVTC	VVDVSH	EDPEVKFNWYD	300
DB	239	LGSPSVFLP	PPPKPOTL	MSRTPEVTC	VVDVSH	EDPEVKFNWYD	298
QY	301	QYNSTYRV	SVSLTVLH	QDWLNK	KEYCKV	SNKALPAPI	360
DB	299	QYNSTYRV	SVSLTVLH	QDWLNK	KEYCKV	SNKALPAPI	358
QY	361	REMTKNQV	SLTCLV	KGFYPSD	IAVWESNG	OPENNYKTP	420
DB	359	REMTKNQV	SLTCLV	KGFYPSD	IAVWESNG	OPENNYKTP	418
QY	421	SRWQGNV	FSCSVW	HEALHNH	YTKSLS	SPGK	453
DB	419	SRWQGNV	FSCSVW	HEALHNH	YTKSLS	SPGK	451

RESULT 12
 US-09-792-938-2
 ; Sequence 2, Application US/09792938
 ; Publication No. US20030166868A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Escho Ekinaduse Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R1
 ; CURRENT APPLICATION NUMBER: US/09/792,938
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 09/282,505
 ; PRIOR FILING DATE: 1999-03-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 2
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-451
 ; OTHER INFORMATION: Sequence is completely synthesized
 US-09-792-938-2

Query Match 97.4%; Score 2369; DB 10; Length 451;
 Best Local Similarity 98.0%; Pred. No. 2.4e-155;
 Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
DB	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYIS	TSYGSNNWIRQAPGKGL	EWVASIT	YDGS	60
QY	61	ADSVKGRFTISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
DB	61	NPSVKGRITISRD	SKNTFYLN	QNSLRRAEDTAVY	CARGSHYF	GHWHFAVWGQGL	120
QY	121	SASTKGKPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	180
DB	121	SAST--KGPSVPL	APSSKSTSG	TAALGCLVKDY	FPPEPVT	VSNWNGALTS	178

QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 240
DB 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 238
QY 241 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
DB 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

RESULT 13
US-10-113-996-18
; Sequence 18, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Gardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-18

Query Match 97.4%; Score 2369; DB 14; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQTLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQTLTVTS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 240
DB 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 238
QY 241 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
DB 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

QY 301 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

RESULT 14
US-10-292-869-2
; Sequence 2, Application US/10292869
; Publication No. US20030158389A1
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/10/292,869
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/282,846
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
US-10-292-869-2

Query Match 97.4%; Score 2369; DB 14; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIROAPGKGLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQTLTVTS 120
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQTLTVTS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
DB 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 240
DB 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVKVPKSCDKTHTCPCPAPL 238
QY 241 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
DB 239 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
QY 301 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
DB 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
DB 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 453
DB 419 SRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 451

RESULT 15

US-09-726-258-71

Sequence 71, Application US/09726258

Publication No. US20030021790A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Heei, Vanessa

APPLICANT: Koumenis, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Shahrokhi, Zahra

APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND

TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/726,258

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/234,182

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/094003

FILING DATE: 24-JUL-1998

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-726-258-71

Query Match 91.1%; Score 2214.5; DB 10; Length 452;

Best Local Similarity 92.7%; Pred. No. 1.1e-144;

Matches 422; Conservative 8; Mismatches 20; Indels 5; Gaps 4;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIRQAPGKGLEWVASI-TYDGGSTN 59

Db 1 EVGLVQSGGGLVQPGGSLRLSCAASGYSPSSHV-MHWVRQAPGKGLEWVGIDPSNGETT 59

QY 60 YADSVKGRFTISDDSKNFTYLQMSLRAEDTAVYICARGSH-YFGHHFAVWGQGLTVT 118

Db 60 YNQKFKGRFTLSRDNSKNTAYLQMSLRAEDTAVYICARGDYRYNGDMFFDVWGQGLTVT 119

QY 119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGVHTPPA 178

Db 120 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGVHTPPA 177

QY 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAP 238

Db 178 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAP 237

QY 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298

Db 238 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 297

299 EQYNSTYRWVSVLTVLHODWLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358

298 EQYNSTYRWVSVLTVLHODWLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 357

359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 418

358 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 417

419 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

418 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452

Search completed: May 13, 2004, 15:56:56

Job time : 53.6587 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:23 ; Search time 18.9031 Seconds

(without alignments)
2305.161 Million cell updates/sec

Title: US-09-925-179-8

Perfect score: 2432

Sequence: 1 EVQLVESGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1750	72.0	330	1 GHU	Ig gamma-1 chain C
2	1625.5	66.8	377	2 A23511	Ig gamma-3 chain C
3	1623.5	66.8	377	2 A60764	Ig gamma-3 chain C
4	1599	65.7	326	1 G2HU	Ig gamma-2 chain C
5	1585.5	65.2	327	1 G4HU	Ig gamma-4 chain C
6	1507.5	62.0	444	2 PC4436	monoclonal antibod
7	1477	60.7	374	2 S69339	Ig heavy chain v r
8	1467	60.3	470	2 S22080	Ig heavy chain pre
9	1444	59.4	472	2 S34459	Ig gamma-1 chain -
10	1403.5	57.7	469	2 S37483	Ig gamma-2a chain
11	1403	57.7	446	2 S40295	Ig gamma-2a chain
12	1359	55.9	474	1 G2XS11	Ig gamma-2b chain
13	1345.5	55.3	475	2 S01321	Ig gamma-2b chain
14	1263	51.9	328	2 I47159	Ig gamma 2a chain
15	1257	51.7	328	2 I47160	Ig gamma 2b chain
16	1254	51.6	255	4 S33866	Ig gamma-1 chain C
17	1248	51.3	234	2 PT0207	Ig gamma-1 chain C
18	1231.5	50.6	323	1 GHRB	Ig gamma chain C r
19	1231	50.6	328	2 I47158	Ig gamma 1 chain c
20	1227	50.5	329	1 I47161	Ig gamma 3 chain c
21	1202.5	49.4	329	1 G2GP	Ig gamma-2 chain C
22	1162.5	47.8	308	2 C30554	Ig heavy chain C r
23	1157	47.6	289	1 G3HUW1	Ig gamma-3 heavy c
24	1150	47.3	326	2 PS0017	Ig gamma-1 chain C
25	1142	47.0	324	1 G1MS	Ig gamma-1 chain C
26	1142	47.0	329	1 G3MSC	Ig gamma-3 chain C
27	1139.5	46.9	333	2 PS0018	Ig gamma-2b chain
28	1137	46.8	333	1 G1MSM	Ig gamma-1 chain C
29	1131	46.5	398	1 G3MSM	Ig gamma-3 chain C

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91568; A91723; A02146

R:Ellison, J.W.; Bersson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the Gim(17) allotypic marker, 97-Lys, and the Gim(1) markers,
A:Note: Lys-330 is removed after translation

R:Harris, L.J.

Submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequ
A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R', 98-135 <CUN>

A:Note: This sequence has the Gim(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ
A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Accession: B90564

A:Molecule type: protein

A:Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, N', 196-197, D', 199-238, E', 240

A:Note: This sequence has the Gim(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein N1e
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'X', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Sevler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Sevler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enonide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) #status experimental
Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred. No. 8.3e-95;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
Qy 122 ASKKGKPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 ASK--KGPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 58
Qy 182 SSGLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELL 118
Qy 242 GGPVSFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKPRBEQ 301
Db 119 GGPVSFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNATKPRBEQ 178
Qy 302 YNSTYRVSVLTVLHODWLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 361
Db 179 YNSTYRVSVLTVLHODWLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 238
Qy 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 298
Qy 422 RWQQGNVFCVSMVHEALHNYTKQSLSPGK 453
Db 299 RWQQGNVFCVSMVHEALHNYTKQSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12959; NID:933070; PIDN:CAA27268.1; PID:9577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMW>
Query Match 66.8%; Score 1625.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 1.7e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;
Qy 122 ASKKGKPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 ASK--KGPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 58
Qy 182 SSGLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVV----- 221
Db 59 SSGLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKVELKTPGLDTHTCPRCPPEK 118
Qy 222 -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK 254
Db 119 SCDTPPPCPRCBPBKSCDTPPPCPRCBPBKSCDTPPPCPRCBPAPPELLGGPSVFLFPPKPK 178
Qy 255 DTLMSIRTPVTCVVDVSHEDPEVKFNWYDGVVHNATKPRBEQYVNSTYRVSVLTV 314
Db 179 DTLMSIRTPVTCVVDVSHEDPEVKFNWYDGVVHNATKPRBEQYVNSTYRVSVLTV 238
Qy 315 LHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR EEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR EEMTKNQVSLTCL 298
Qy 375 VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQGNVFCVSM 434
Db 299 VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQGNVFCVSM 358
Qy 435 HEALHNYTKQSLSPGK 453
Db 359 HEALHNYTKQSLSPGK 377
RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
A:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conver
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMW>

Query Match 66.8%; Score 1623.5; DB 2; Length 377;
 Best Local Similarity 82.1%; Pred. No. 2.2e-87;
 Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGGKPSVFLAPSSKSTSGTAALGCLVDPPEPTVTVSWNSGALTSVHTTFAVLQ 181
 DB 1 AST--KGPSVFLAPCSRSTSGTAALGCLVDPPEPTVTVSWNSGALTSVHTTFAVLQ 58

QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKV----- 221
 DB 59 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVELKTLPLDTHTCPCPCPK 118

QY 222 -----EPKSCDKTHTCPCPAPPELLGSPSVFLPPPK 254
 DB 119 SCDTPPCPCPKSCDTPPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPC 178

QY 255 DTLIMISRTPTVTCVVDVSHEDPEVFNWVGVVHNAKTPREQYNSTYRVSVLT 314
 DB 179 DTLIMISRTPTVTCVVDVSHEDPEVFNWVGVVHNAKTPREQYNSTYRVSVLT 238

QY 315 LHQDWLNGKEYKCVKSNKALPAPIETIKSAKQPREPOVYTLPPSREMTKNQVSLTCL 374
 DB 239 LHQDWLNGKEYKCVKSNKALPAPIETIKSAKQPREPOVYTLPPSREMTKNQVSLTCL 298

QY 375 VKGFYPSDIAVESNGQPNNTTPPVLDSGSPFLYKSLTVDKSRWQGNVFCSCVM 434
 DB 299 VKGFYPSDIAVESNGQPNNTTPPVLDSGSPFLYKSLTVDKSRWQGNVFCSCVM 358

QY 435 HEALHNYTKQSLSLSPGK 453
 DB 359 HEALHNYTKQSLSLSPGK 377

RESULT 4
 G2HU
 Ig gamma-2 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
 C;Accession: A93906; A92809; A93132; A02148
 R;Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 A;Reference number: A93906; MUID:82197621; PMID:6804948
 A;Accession: A93906
 A;Molecule type: DNA
 A;Residues: 1-326 <ELL>
 A;Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056
 A;Note: Lys-326 is probably removed posttranslationally
 R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
 A;Reference number: A92809; MUID:81007873; PMID:6774012
 A;Contents: myeloma protein Til
 A;Accession: A92809
 A;Molecule type: Protein
 A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A;Note: Trp-156 is at or near the complement-binding site
 R;Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A;Title: The amino acid sequences of the three heavy chain constant region domains of a
 A;Reference number: A90752; MUID:80001357; PMID:113060
 A;Contents: myeloma protein Zie
 A;Accession: A90752
 A;Molecule type: Protein
 A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A;Note: this sequence has since been revised
 R;Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A;Reference number: A93132; MUID:80114419; PMID:118920
 A;Contents: Zie
 A;Accession: A93132

A;Molecule type: protein
 A;Residues: 238-275 <HOF>
 R;Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A;Reference number: A94591
 A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
 ned
 R;Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A;Reference number: A90533; MUID:72033500; PMID:4940472
 A;Contents: annotation; myeloma protein Sa, disulfide bonds
 R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:69064124; PMID:5782707
 A;Contents: annotation; Sa, disulfide bonds
 C;Genetics:
 A;Gene: GDB:IGHG2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q32.33-14q32.33
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) k
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into]
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;133-202/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,140-200,246-304/Disulfide bonds: #status experimental
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.7%; Score 1599; DB 1; Length 326;
 Best Local Similarity 91.3%; Pred. No. 4.9e-86;
 Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;

QY 122 ASTKGGKPSVFLAPSSKSTSGTAALGCLVDPPEPTVTVSWNSGALTSVHTTFAVLQ 181
 DB 1 AST--KGPSVFLAPCSRSTSGTAALGCLVDPPEPTVTVSWNSGALTSVHTTFAVLQ 58

QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKVPCDKTHTCPCPAPPELL 241
 DB 59 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVERKCCVE---CPCPAPP-V 114

QY 242 GGFPSVFLPPPKDTLMISRTPTVTCVVDVSHEDPEVFNWVGVVHNAKTPREEQ 301
 DB 115 AGPSVFLPPPKDTLMISRTPTVTCVVDVSHEDPEVFNWVGVVHNAKTPREEQ 174

QY 302 YNSTYRVSVLTVLHODWLNCKEYKCVKSNKALPAPIETIKSAKQPREPOVYTLPPSR 361
 DB 175 FNSTFRVSVLTVLHODWLNCKEYKCVKSNKALPAPIETIKSAKQPREPOVYTLPPSR 234

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVESNGQPNNTTPPVLDSGSPFLYKSLTVDKS 421
 DB 235 EEMTKNQVSLTCLVKGFYPSDIAVESNGQPNNTTPPVLDSGSPFLYKSLTVDKS 294

QY 422 RWQGNVFCSCVMHEALHNYTKQSLSLSPGK 453
 DB 295 RWQGNVFCSCVMHEALHNYTKQSLSLSPGK 326

RESULT 5
 G4HU
 Ig gamma-4 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
 C;Accession: A90933; A90249; A02150
 R;Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: The sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant z
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Interons: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 65.2%; Score 1585.5; DB 1; Length 327;
Best Local Similarity 91.0%; Pred. No. 3e-85;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;
QY 122 ASTKGGPSVFLPAPSKSTGGTAAALGCLVDPYEPVTVSWNSGALTSVHTTPAVLQ 181
DB 1 AST--KGPSVFLPAPCRSTSSSTAALGCLVDPYEPVTVSWNSGALTSVHTTPAVLQ 58
QY 182 SSGLYSLSSVTVVPSSSLGTQYICNVNKKPSNTKVDKVPKSCDKTHTCPAPPELL 241
DB 59 SSGLYSLSSVTVVPSSSLGTQYICNVNKKPSNTKVDKVPKSCDKTHTCPAPPELL 115
QY 242 GGPVSFLPFPKPKDTLWISRTPEVTCVVDVSHEDPEVKFNVDGVVHNKTKPREQ 301
DB 116 GGPVSFLPFPKPKDTLWISRTPEVTCVVDVSHEDPEVKFNVDGVVHNKTKPREQ 175
QY 302 YNSTYRVSVVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
DB 176 FNSTYRVSVVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 235
QY 362 EEMTKQVSLTCLVKGYPDSIAVWESNGQPNNTKTPPVLDSDGSFLLSKLTVDSK 421
DB 236 EEMTKQVSLTCLVKGYPDSIAVWESNGQPNNTKTPPVLDSDGSFLLSKLTVDSK 295
QY 422 RWQGNVFCVSNVMEALHNHYTKSLSPGK 453
DB 296 RWQGNVFCVSNVMEALHNHYTKSLSPGK 327
RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
R:Kashii, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yanaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphy
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C:Superfamily: immunoglobulin C region; immunoglobulin homology

F;251-320/Domain: immunoglobulin homology <IM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted
Query Match 62.0%; Score 1507.5; DB 2; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.4e-80;
Matches 284; Conservative 67; Mismatches 86; Indels 23; Gaps 9;
QY 1 EVLVESGGGLVQPGGSLRLSCAIVGYSITSYSNWIRQAPGKGLWVASITYDG---S 57
DB 1 EVQVETGGGLVQPGGSLRLSCAIVGYSITSYSNWIRQAPGKGLWVASITYDG---S 57
QY 58 TNYADSVKGRFTISRDDSKNTFYLQNSLRRAEDTAVYVCARGSHYFGHHFAV--WGQQT 115
DB 60 AKYAESVGRFTISRDDSKNTFYLQNSLRRAEDTAVYVCARGSHYFGHHFAV--WGQQT 114
QY 116 LVTVSASTKGGPSVFLPAPSKSTGGTAAALGCLVDPYEPVTVSWNSGALTSVHT 175
DB 115 SVTVSSAKT--TPPSVYPLAPSAQTSMTLGLVKGYPFPEVTVTVNSGSLSGVHT 172
QY 176 FPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNKKPSNTKVDKVPKSCDKTHTCP 234
DB 173 FPAVLQSD--LYTLSSSVTVVPSSSTWPSSETVTCNVHPASSTKVDKIVPRDCG----CKPC 227
QY 235 -CPAPELLOGPSVFLPFPKPKDTLWISRTPEVTCVVDVSHEDPEVKFNVDGVVHN 293
DB 228 ICTVPEV---SSVFIPEPKPKDVLITLTPKVTCTVVDVSHEDPEVKFNVDGVVHN 284
QY 294 KTVPRSEQVNSTYRVSVVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREQ 353
DB 285 QTQPREQVNSTYRVSVVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREQ 344
QY 354 VYTLPPSRREMTKNQVSLTCLVKGYPDSIAVWESNGQPNNTKTPPVLDSDGSFLL 413
DB 345 VYTLPPSRREMTKNQVSLTCLVKGYPDSIAVWESNGQPNNTKTPPVLDSDGSFLL 404
QY 414 SKLTVDSKSRVQGNVFCVSNVMEALHNHYTKSLSPGK 453
DB 405 SKLTVDSKSRVQGNVFCVSNVMEALHNHYTKSLSPGK 444
RESULT 7
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 60.7%; Score 1477; DB 2; Length 374;
Best Local Similarity 63.5%; Pred. No. 7e-79;
Matches 289; Conservative 20; Mismatches 44; Indels 102; Gaps 3;
QY 1 BVQVLESGGGLVQPGGSLRLSCAIVGYSITSYSNWIRQAPGKGLWVASITYDGSTN 59
DB 20 QITLKESGPTLVKXTQITLTCTTSGLSKSGVGVGWIRQPPGQALWLAIFWDDDKR 79

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QY 60 YADSVKGRFTISRDDSKNTFYLQMSLRRAEDTAVYYCARGSHYFGH-WHEFAVWGQGLT 118
Db 80 YPSLRLTRITIKDTSKQVLTWNVDPADTATYTCGVSGVGGGRFHSHWGQGLT 139
QY 119 VSSASTKGKPSVFPPLAPSKSTSGGTAALGLVKDYFPEPVTVSNMGALTSVGHVTPPA 178
Db 140 VSS----- 142
QY 179 VLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCPAP 238
Db 143 -----EPKSCDKTHTCPCPAP 159
QY 239 ELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPR 298
Db 160 ELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPR 219
QY 299 EQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVYTL 358
Db 220 EQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVYTL 279
QY 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTV 418
Db 280 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTV 339
QY 419 DKSRWQGNVFCVSNVHEALHNHYTQKSLSLSPGK 453
Db 340 DKSRWQGNVFCVSNVHEALHNHYTQKSLSLSPGK 374

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RESULT 8
S22080
Ig heavy chain precursor (B/Wt.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match 60.3%; Score 1467; DB 2; Length 470;
Best Local Similarity 62.6%; Pred. No. 3.5e-78;
Matches 286; Conservative 58; Mismatches 103; Indels 10; Gaps 8;

QY 1 EVQLVSGGGLVQPGSRLRSCAVGSYISITGSYNNWIRQAPGKLEWVASITYDGSNTY 60
Db 20 QVLRSGGGLVQPGSRLRSCAVGSYISITGSYNNWIRQAPGKLEWVASITYDGSNTY 78
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRRAEDTAVYYCARGSH-YFGHWEFA-VWGQGLT 118
Db 79 NPALKSRLSITKENSQVSLSVSYTPEDTATYYCARSTYGEVGDGADAWGQGLT 138

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QY 119 VSSASTKGKPSVFPPLAPSKSTSGGTAALGLVKDYFPEPVTVSNMGALTSVGHVTPPA 178
Db 139 VSSAST--TAPKVYPLSSCCGSKSSVTGLCLVSSVMPPEVTVWNSGALKSGVHTFPA 196
QY 179 VLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCPAP 238
Db 197 VLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCPAP 253
QY 239 ELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPR 298
Db 254 ELPGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPR 313
QY 299 EQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVYTL 358
Db 314 EQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVYTL 373
QY 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSLK 416
Db 374 PQBELSKSTVSITCMWTSFYDPYIAVEWQNGQPSSEDKYGTTPPOLDADSSFYLYSKL 433
QY 417 TVDKSRNQGNVFCVSNVHEALHNHYTQKSLSLSPGK 453
Db 434 RVDNSNQEGDITTCVVMHEALHNHYTQKSTKSAGK 470

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RESULT 9
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patrici, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match 59.4%; Score 1444; DB 2; Length 472;
Best Local Similarity 59.9%; Pred. No. 7.5e-77;
Matches 275; Conservative 64; Mismatches 110; Indels 10; Gaps 5;

QY 1 EVQLVSGGGLVQPGSRLRSCAVGSYISITGSYNNWIRQAPGKLEWVASITYDGSNTY 60
Db 18 QVLRQESGPSLATLLQTLSTVITISGFSL--NNYGVDMVRQAPGKALEWLGSGYDEIDY 76
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRRAEDTAVYYCAR---GSHYFGHWEFAVWGQGL 116
Db 77 NPVLKSLRSLTKDTSKQVSLTSTVTEDTAVYYCARVDYDSSHAPAYASYDFWGPGLL 136
QY 117 VTSSASTKGKPSVFPPLAPSKSTSGGTAALGLVKDYFPEPVTVSNMGALTSVGHVTF 176
Db 137 ISVLAST--TPPKVYELTSCCGDTSSTSSIVTGLCLVSSVMPPEVTVWNSGALTSVGHVTF 194
QY 177 PAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCP 236
Db 195 PAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCP 253
QY 237 APELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATK 296
Db 254 PPELLGGPSVFLFPKPKDITLTISGTEVTCVVVDVQDDPEVQFSFVNDVNEVTRATK 313
QY 297 PREQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVY 356
Db 314 PREQYNSTYRVVSVLTVTHQDMLNGKEYCKKVSNNKALPAIEKTIISKAKQPREPQVY 373
QY 357 LPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSL 414

```

Db 374 LAPPEELSKTSLVCTLVTFYDYIAVEWQKQPESEKYGITTSQLDADGSFLYS 433
QY 415 KLTVDKSRWQGNVFCSSVMHEALHNHYTKSLSPGK 453
Db 434 RLRVDKNSWQEGDTYACVVMHEALHNHYTKSLSPGK 472

RESULT 10
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMV>

Query Match 57.7%; Score 1403.5; DB 2; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.7e-74;
Matches 270; Conservative 68; Mismatches 102; Indels 23; Gaps 8;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGSYNNWIRQAPGKLEWVASI-TYDGSN 59
Db 20 QIQLOQSGPELVKPGASVKISCKASGYTFD-YIHWKQPGQGLGWIGWYFASGNTK 78
QY 60 YADSVKGRFTISRDPSKNTFYLMNSLRADTAIVYVYCARGS-----HYFGHWHPAVWG 112
Db 79 YNENFKGKATLVDTSSSTAYVQLSSLTSEDVAVYFCARAMGATATLLDY-----WG 130
QY 113 QGLTVTSASAKGKGPVFPPLAPSSKSTSGTAAALGLVQDYPPPEVTVSNWNSGALTSG 172
Db 131 QGTTLTVSSAKT--TAPSYIPLAPVCGDTTGSVTLGLVKGYPPEPVTLLTWNSSGSSG 188
QY 173 VHTFPAVLQSD-LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPC 246
Db 189 VHTFPAVLQSD-LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPC 246
QY 233 TP--CPAPELLGGPSVFLPPPKPKOTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEV 290
Db 247 PPKCPAPNLLGGPSVFLPPPKPKOTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEV 306
QY 291 HNAKTPREEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIERTISKPGSVRAPOVYV 350
Db 307 HTAQCTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKOLPAPIERTISKPGSVR 366
QY 351 EQQVTLPPSREMTKNQVSLTCLVKGYPSPDIWESNGOPENNYKTTTPVLDSDGSP 410
Db 367 APQVYVLPPEEMTKKQVTLTCMTVDFMPEDIVYVETWNGKTELNYKNTPEVLDSDGSY 426
QY 411 FLYSKLTVDKSRWQGNVFCSSVMHEALHNHYTKSLSPGK 453
Db 427 FNYSKLRVEKKNWERNISCSVWHEGLNHHHTTKSPSRTPGK 469

RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Prosch, M.; Weisgerber, C.; B.
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295

A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH2>
F:118-446/Domain: C1 region <CH1>
F:118-214/Domain: hinge
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMV>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:22-96, 144-199, 261-321, 367-425/Disulfide bonds: #status predicted
F:322/Disulfide bonds: interchain (to light chain) #status predicted
F:224, 227, 229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.7%; Score 1403; DB 2; Length 446;
Best Local Similarity 59.4%; Pred. No. 1.7e-74;
Matches 271; Conservative 67; Mismatches 104; Indels 14; Gaps 8;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGSYNNWIRQAPGKLEWVASI-TYDGS--T 58
Db 1 QIQLOQSGPELVKPGASVKISCKASGYTFD-YIHWKQPGQGLGWIGWYFASGNT 58
QY 59 YADSVKGRFTISRDPSKNTFYLMNSLRADTAIVYVYCARGSYFPGHWFAVWGQTLVT 118
Db 59 KYNEKFKGKATLVDTSSSTAYVQLSSLTSEDVAVYFCARG---GKFAMDYWGQTSVT 114
QY 119 VSSASTKGKGPVFPPLAPSSKSTSGTAAALGLVQDYPPPEVTVSNWNSGALTSGVHTFPA 178
Db 115 VSSAKT--TAPSYIPLAPVCGDTTGSVTLGLVKGYPPEPVTLLTWNSSGSSGVT 172
QY 179 VLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKNTKVDKVEPKSCDKHTCCP--CP 236
Db 173 VLQSD-LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPKCP 230
QY 237 APPELLGGPSVFLPPPKPKOTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTK 296
Db 231 APNLLGGPSVFLPPPKPKOTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTK 290
QY 297 PREEQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIERTISKAGQPREPQVYV 356
Db 291 THREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKOLPAPIERTISKPGSVRAPOVYV 350
QY 357 LPPSREMTKNQVSLTCLVKGYPSPDIWESNGOPENNYKTTTPVLDSDGSPFLYSKL 416
Db 351 LPPPEEMTKKQVTLTCMTVDFMPEDIVYVETWNGKTELNYKNTPEVLDSDGSPFMYSKL 410
QY 417 TVDKSRWQGNVFCSSVMHEALHNHYTKSLSPG 452
Db 411 RVBKQWERNISCSVWHEGLNHHHTTKSPSRTPG 446

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A:Reference number: S25057
A:Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827

R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
 A;Reference number: A02157; MUID:80120716; PMID:6766534
 A;Contents: a allele
 A;Accession: A02157
 A;Molecule type: DNA
 A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
 A;Cross-references: GB:J00461
 A;Note: the sequence was determined from the germline gene
 R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
 A;Reference number: A26235; MUID:80081501; PMID:117548
 A;Contents: MPC 11
 A;Accession: A26235
 A;Molecule type: mRNA
 A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
 A;Note: Lys-474 is probably removed posttranslationally
 R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
 A;Reference number: A26232; MUID:80081502; PMID:117549
 A;Accession: A26232
 A;Molecule type: DNA
 A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
 R;Olo, R.; Rougson, F.
 Nature 296, 761-763, 1982
 A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
 A;Reference number: A26233; MUID:82173203; PMID:6903173
 A;Contents: b allele
 A;Accession: A26233
 A;Molecule type: DNA
 A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A;Cross-references: GB:J00461
 R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
 J. Biol. Chem. 269, 12345-12350, 1994
 A;Title: O-glycosylation in hinge region of mouse immunoglobulin g2b.
 A;Reference number: A53598; MUID:94216359; PMID:7512967
 A;Accession: A53598
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 234-251 <KIN>
 C;Comment: The a allele sequence is shown.
 C;Genetics:
 A;Introns: 138/1; 236/1; 258/1; 368/1
 C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kap
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglob
 F;157-222/Domain: immunoglobulin homology <IM1>
 F;236-257/Region: hinge
 F;281-350/Domain: immunoglobulin homology <IM2>
 F;387-454/Domain: immunoglobulin homology <IM3>
 F;152/disulfide bonds: interchain (to light chain) #status predicted
 F;154-220,288-348,394-452/disulfide bonds: #status predicted
 F;247,250,253,256/disulfide bonds: interchain (to heavy chain) #status predicted
 F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 55.9%; Score 1359; DB 1; Length 474;
 Best Local Similarity 56.7%; Pred. No. 6,6e-72;
 Matches 262; Conservative 71; Mismatches 113; Indels 16; Gaps 8;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNWIRQAPGKLEWVASI--TYDGT 58
 DB 20 EVQLQQSGPELVNPGASVKMSCKASGYTFIT-YMHWVKQPGQGLEWIGYINPNKDG-T 77
 QY 59 NYADSVKGRFTISRDSSKNTFYLQVNSLRSEDYAVYTCARGSHYFGHWHFAVWGQGLT 118
 DB 78 KFNKFKGKATLTDKSNATYMSLSLTSEDSAVYTCARDY--DW-FAYWGQGLT 134
 QY 119 VSSASTKGKGVSPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178

DB 135 VSAKT--TPPSVYPLAPGCGDITGSSVTSGCLVKGYPPEVSVTVTNWNSGLSSSVHTLSQ 192
 QY 179 VLOSSGLYSLSSVTVYVSSSLGTOTICNVNHNKPSNTKVDKVPKSCDKT-HTCPEP--- 234
 DB 193 ALIQSGLYTMSSTVYVSSVTPSQVTCVAHFASSSTVVDKLEPSGPISTINPCPCKE 252
 QY 235 ---CPAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVH 291
 DB 253 CHKCPAPNLEGSPSVFIFFPNIKDVLMIISLTPTKVTCVVDVSDDDPDVQISWVNNVEVH 312
 QY 292 NAKTKPREEQNSTYRVVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAKGP 351
 DB 313 TAQOTHRDYNSTIRVSVTLFQHQDMKSGKFKCKVNNKDLPSPIERTISKIGLVRA 372
 QY 352 PQVYILPPSREEMTKNQVSLTCLVKGYPSPDIKAVESNQGPNNTPTPPVLDSDGSPFF 411
 DB 373 PQVYILPPPAEQLSRKQVSLTCLVGFNPGDISEVWTSNGTEENTKDTAPVLDSDGSYF 432
 QY 412 LYSKLTVDKRWQGNVFCVSNVHEALHNHYTKSLSPGK 453
 DB 433 IYSKLNKTKWEKTDSDFCNVRHEGLKNVYKTKTISRSPGK 474
 RESULT 13
 S01321
 Ig gamma-2b chain precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C;Accession: S01321
 R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, P.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
 A;Reference number: S01320; MUID:98329081; PMID:3138116
 A;Accession: S01321
 A;Molecule type: mRNA
 A;Residues: 1-475 <DEI>
 A;Cross-references: EMBL:X13188; NID:g51780; PID:CAA1580.1; PID:g51781
 A;Note: this sequence was determined from the differentiated gene
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F;159-223/Domain: immunoglobulin homology <IM1>
 Query Match 55.3%; Score 1345.5; DB 2; Length 475;
 Best Local Similarity 56.7%; Pred. No. 4e-71;
 Matches 262; Conservative 72; Mismatches 113; Indels 15; Gaps 8;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNWIRQAPGKLEWVASIYDGTN- 59
 DB 20 QVQLQQSGAEARPGASVKLSCKASGYTLTS-YGISWVKQRTGGGLEWIGEI-YPGSGNS 77
 QY 60 -YADSVKGRFTISRDSSKNTFYLQVNSLRSEDYAVYTCARGSHYFGHWHFAVWGQGLT 118
 DB 78 YFNEKFKGKATLTDKSNSTAYLHLSLTSEDSAVYFCA-GPRQVGLLPFGYWGQGLT 136
 QY 119 VSSASTKGKGVSPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
 DB 137 ASAAT--TPPSVYPLAPGCGDITGSSVTLCGLVKGYFPPEVTVTNWNSGLSSSVHTFPA 194
 QY 179 VLOSSGLYSLSSVTVYVSSSLGTOTIYCNVNHKPSNTKVDKVPKSCDKT-HTCPEP--- 234
 DB 195 LLO-SGLYTMSSVTVPSSTVPSQVTCVAHFASSSTVVDKLEPSGPTSTINPCPCKE 253
 QY 235 ---CPAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVH 291
 DB 254 CHKCPAPNLEGSPSVFIFFPNIKDVLMIISLTPTKVTCVVDVSDDDPDVQISWVNNVEVL 313
 QY 292 NAKTKPREEQNSTYRVVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAKGP 351
 DB 314 TAQOTHRDYNSTIRVSVTLFQHQDMKSGKFKCKVNNKDLPSPIERTISKIGLVRA 373
 QY 352 PQVYILPPSREEMTKNQVSLTCLVKGYPSPDIKAVESNQGPNNTPTPPVLDSDGSPFF 411

Db 374 PQVYLSPPQLSRKDVSLTCLAVGSPEDISVEWTSNGHTENYKDTAPVLDSDGSYF 433
 QY 412 LYSKLTVDKSWQOQNFVSCSWHEALHNHYTKSLSLSPCK 453
 Db 434 IYKLNMTSKWEKIDFSFCNVRHEGLKNYLYLKIISRSPOK 475

RESULT 14
 I47159
 Ig gamma 2a chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47159
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47159
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
 C:Genetics:
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMW>

Query Match 51.9%; Score 1263; DB 2; Length 328;
 Best Local Similarity 70.3%; Pred. No. 1.7e-66;
 Matches 230; Conservative 43; Mismatches 48; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTPDAVLQSSGLYSYL 188
 Db 6 PLVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVWNSGALTSGVHTFPPSVLPQSLYSYL 65

QY 189 SSVTVVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCCPPAPPELLGGPSVFL 248
 Db 66 SSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGKTKPPCPICPACESP----GPSVFI 121

QY 249 FPKPKDITLMISRTPEVTCVVDVSHDEPEVKFNWYVGVVHNKTKPRBEQYNSTYRV 308
 Db 122 FPKPKDITLMISRTPEVTCVVDVSHDEPEVKFNWYVGVVHNKTKPRBEQYNSTYRV 181

QY 309 VSVLTVLHODWLNKGEYKCKVSNKALPAPIETIKSKAQGPPEQVYTLPPSREMTKNQ 368
 Db 182 VSVLPIQHODWLNKGEYKCKVSNKALPAPIETIKSKAQGPPEQVYTLPPHAEELSRSK 241

QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSFELYSKLTVDKSRWQOG 426
 Db 242 VSIITCLVIGFYPPDIDVEWQNGQPEPEGNRYRTTPQDDVDGTYFLYSKFSVDKASWQOG 301

QY 427 NVFSCSWHEALHNHYTKSLSLSPCK 453
 Db 302 GIFQCAVMEALHNHYTKSISKTPOK 328

Search completed: May 13, 2004, 15:48:01
 Job time : 19.9031 secs

A:Gene: IgG2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMW>

Query Match 51.7%; Score 1257; DB 2; Length 328;
 Best Local Similarity 70.0%; Pred. No. 3.7e-66;
 Matches 229; Conservative 42; Mismatches 50; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTPDAVLQSSGLYSYL 188
 Db 6 PLVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVWNSGALTSGVHTFPPSVLPQSLYSYL 65

QY 189 SSVTVVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKHTHTCCPPAPPELLGGPSVFL 248
 Db 66 SSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGKTKPPCPICPACESP----GPSVFI 121

QY 249 FPKPKDITLMISRTPEVTCVVDVSHDEPEVKFNWYVGVVHNKTKPRBEQYNSTYRV 308
 Db 122 FPKPKDITLMISRTPEVTCVVDVSHDEPEVKFNWYVGVVHNKTKPRBEQYNSTYRV 181

QY 309 VSVLTVLHODWLNKGEYKCKVSNKALPAPIETIKSKAQGPPEQVYTLPPSREMTKNQ 368
 Db 182 VSVLPIQHODWLNKGEYKCKVSNKALPAPIETIKSKAQGPPEQVYTLPPHAEELSRSK 241

QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSFELYSKLTVDKSRWQOG 426
 Db 242 VSIITCLVIGFYPPDIDVEWQNGQPEPEGNRYRTTPQDDVDGTYFLYSKFSVDKASWQOG 301

QY 427 NVFSCSWHEALHNHYTKSLSLSPCK 453
 Db 302 GIFQCAVMEALHNHYTKSISKTPOK 328

Search completed: May 13, 2004, 15:48:01
 Job time : 19.9031 secs

RESULT 15
 I47160
 Ig gamma 2b chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
 C:Genetics:

Db 374 PQVYLSPPQLSRKDVSLTCLAVGSPEDISVEWTSNGHTENYKDTAPVLDSDGSYF 433
 QY 412 LYSKLTVDKSWQOQNFVSCSWHEALHNHYTKSLSLSPCK 453
 Db 434 IYKLNMTSKWEKIDFSFCNVRHEGLKNYLYLKIISRSPOK 475

RESULT 15
 I47160
 Ig gamma 2b chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
 C:Genetics:

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:10:58 ; Search time 14.1773 Seconds
(without alignments)
1663.785 Million cell updates/sec

Title: US-09-925-179-8

Perfect score: 2432

Sequence: 1 EVQLVESGGGLVPGGSLRL.....MHEALHNYTKSLSPGK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1750	72.0	330	1 GC1_HUMAN	P01857 homo sapien
2	1599	65.7	326	1 GC2_HUMAN	P01859 homo sapien
3	1585.5	65.2	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	50.6	323	1 GC4_RABIT	P01870 oryctolagus
5	1202.5	49.4	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	47.8	290	1 GC1_HUMAN	P01860 homo sapien
7	1150	47.3	326	1 GC1_MOUSE	P20759 rattus norv
8	1142	47.0	324	1 GC1_MOUSE	P01868 mus musculus
9	1142	47.0	329	1 GC3_MOUSE	P22436 mus musculus
10	1139.5	46.9	333	1 GCB_RAT	P20761 rattus norv
11	1137	46.8	393	1 GC1W_MOUSE	P01869 mus musculus
12	1131	46.5	398	1 GC3W_MOUSE	P03987 mus musculus
13	1126	46.3	330	1 GC4A_MOUSE	P01863 mus musculus
14	1123.5	46.2	335	1 GCAB_MOUSE	P01864 mus musculus
15	1121	46.1	399	1 GCAM_MOUSE	P01865 mus musculus
16	1117.5	45.9	329	1 GCC_RAT	P20762 rattus norv
17	1110	45.6	322	1 GCA_RAT	P20760 rattus norv
18	1082	44.5	336	1 GCB_MOUSE	P01866 mus musculus
19	1077	44.3	405	1 GCB_MOUSE	P01867 mus musculus
20	482.5	19.8	429	1 EPC_RAT	P01855 rattus norv
21	478	19.7	428	1 EPC_HUMAN	P01854 homo sapien
22	468	19.2	421	1 EPC_MOUSE	P06336 mus musculus
23	441	18.1	454	1 MUC_HUMAN	P01871 homo sapien
24	439.5	18.0	122	1 HV3G_HUMAN	P01768 homo sapien
25	437.5	18.0	458	1 MUC_RABIT	P03988 oryctolagus
26	431.5	17.7	455	1 MUC_MOUSE	P01872 mus musculus
27	427.5	17.6	476	1 MUCM_RABIT	P04221 oryctolagus
28	421.5	17.3	479	1 MUCM_MOUSE	P01873 mus musculus
29	421	17.3	119	1 HV3I_HUMAN	P01770 homo sapien
30	420	17.3	123	1 HV24_MOUSE	P01793 mus musculus
31	419	17.2	120	1 HV3E_HUMAN	P01766 homo sapien
32	418	17.2	457	1 MUC_SUNMU	P20768 suncus muri
33	415.5	17.1	114	1 HV3B_HUMAN	P01763 homo sapien

34	414	17.0	450	1 MUC_CANFA	P01874 canis famil
35	413.5	17.0	454	1 MUC_WESAU	P06337 mesocricetu
36	413	17.0	121	1 HV3J_HUMAN	P01771 homo sapien
37	412	16.9	115	1 HV3F_HUMAN	P01767 homo sapien
38	410	16.9	115	1 HV3D_HUMAN	P01765 homo sapien
39	408.5	16.7	116	1 HV05_CARAU	P19181 carassius a
40	405.5	16.7	122	1 HV3H_HUMAN	P01769 homo sapien
41	405	16.7	123	1 HV22_MOUSE	P01791 mus musculu
42	404.5	16.6	116	1 HV3T_HUMAN	P01781 homo sapien
43	403.5	16.6	120	1 HV3U_HUMAN	P01782 homo sapien
44	403	16.6	113	1 HV3O_MOUSE	P01799 mus musculu
45	403	16.6	391	1 MUCB_HUMAN	P04220 homo sapien

ALIGNMENTS

RESULT 1					
GC1_HUMAN					
ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.	
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Ig gamma-1 chain C region.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Ellison J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RA	Waxdal M.J., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino				
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";				
RL	Biochemistry 9:3161-3170(1970).				
RN	[3]				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RA	Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino				
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";				
RL	Biochemistry 9:3171-3181(1970).				
RN	[4]				
RP	SEQUENCE (MYELOMA PROTEIN NIE).				
RX	MEDLINE=77070269; PubMed=826475;				
RA	Ponstingl H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a				
RT	monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The				
RT	chymotryptic peptides of the H-chain, alignment of the tryptic				
RT	peptides and discussion of the complete structure.";				
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RN	[5]				
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RX	MEDLINE=83289131; PubMed=6884994;				
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RT	"Three-dimensional structure determination of antibodies. Primary				
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";				
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RN	[6]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC GIM(3) marker and the GIM (non-1) markers.
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of
 CC 35, 116, 198, 289 and 272.
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
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 CC -----
 CC ENBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR PDB; 1AJ7; 12-NOV-97.
 DR PDB; 1DSB; 09-FEB-00.
 DR PDB; 1DS7; 09-FEB-00.
 DR PDB; 1DSV; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1H2H; 12-JUN-02.
 DR PDB; 1I72; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 3D-structure. 1 1
 XW NON_TER 1 1
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.

FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	INTERCHAIN (WITH LIGHT CHAIN).
FT	DISULFID	103	103	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	112	112	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	250	308	N-LINKED (GLCNAC...).
FT	CARBOHYD	180	180	REMOVED POST-TRANSLATIONALLY.
FT	MOD_RES	330	330	K -> R (IN GIM(3) MARKER).
FT	VARIANT	97	97	/FTId=VAR_003886.
FT	VARIANT	239	239	D -> E (IN GIM(NON-1) MARKER).
FT	VARIANT	241	241	/FTId=VAR_003887.
FT	VARIANT	241	241	L -> M (IN GIM(NON-1) MARKER).
FT	VARIANT	241	241	/FTId=VAR_003888.
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	147	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	166	
FT	TURN	168	171	
FT	STRAND	176	179	
FT	TURN	180	181	
FT	STRAND	182	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	260	265	
FT	STRAND	270	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	305	312	
FT	TURN	313	314	
FT	TURN	316	317	
FT	STRAND	320	325	
SEQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match	72.0%;	Score 1750;	DB 1;	Length 330;	
Best Local Similarity	98.8%;	Pred. No. 4.7e-112;			
Matches 328;	Conservative	2;	Mismatches 0;	Indels 2;	Gaps 1;

Qy	122	ASTKGKGPSVFPPLAPSSKSTSGGTAAALGCLVVDYFPEPVTVSNWNSGALTSGVHTFPVLQ	181
Db	1	AST--KGPSVFPPLAPSSKSTSGGTAAALGCLVVDYFPEPVTVSNWNSGALTSGVHTFPVLQ	58
Qy	182	SSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELL	241
Db	59	SSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELL	118
Qy	242	GGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ	301
Db	119	GGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ	178
Qy	302	YNSTYRVVSVLTVQLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR	361
Db	179	YNSTYRVVSVLTVQLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSR	238
Qy	362	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLVDS	421
Db	239	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLVDS	298

QY 422 RWOQGVFSCVMHEALNHYTQKSLSPGK 453
 DB 299 RWOQGVFSCVMHEALNHYTQKSLSPGK 330

RESULT 2
 GC2_HUMAN
 ID GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988 (1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family";
 RL Cell 29:671-679 (1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Kravinkel U., Rabbits T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes";
 RL EMBO J. 1:403-407 (1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications";
 RL J. Immunol. 125:1048-1054 (1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein";
 RL Can. J. Biochem. 57:758-767 (1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains";
 RL Mol. Immunol. 16:923-925 (1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95252598; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins";

Eur. J. Biochem. 228:886-893 (1995).
 [9]
 RN DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2";
 RL Biochem. J. 121:217-225 (1971).
 RN [10]
 RN DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G";
 RL Nature 221:145-148 (1969).
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 CC
 DR EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSP; P01857; IFC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00835; IG LIKE; 3.
 DR PROSITE; PS00290; IG MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 98 CHI.
 FT DOMAIN 1 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 C -> S (IN REF. 3).
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 Query Match 65.7%; Score 1599; DB 1; Length 326;
 Best Local Similarity 91.3%; Pred. No. 8.6e-102;
 Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;
 QY 122 ASTKGKGPSVFPPLAPSKTSSTGTAALGCLVKDYPPEPVTVSNVSGALTSVHTTFAVLQ 181
 DB 1 AST--KGPSVFPPLAPSKTSSTGTAALGCLVKDYPPEPVTVSNVSGALTSVHTTFAVLQ 59
 QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVKPKSCDKTHTCTPCPAPELL 241
 DB 59 SSGLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKVERKCCVE---CPFCAPP-V 114
 QY 242 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNVTVDGVVHNATKPREQ 301
 DB 115 AGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVVHNATKPREQ 174

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QY 302 YNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
DB 175 FNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSR 234
QY 362 EMTKQVSLTCLVKGFPSPDIWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 421
DB 235 EMTKQVSLTCLVKGFPSPDIWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 294
QY 422 RWQGNVSCSVNHEALHNHYTKLSLSPGK 453
DB 295 RWQGNVSCSVNHEALHNHYTKLSLSPGK 326

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1ADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TPR 1 98
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EBDB811EF208E7A CRC64;

Query Match
Best Local Similarity 91.0%; Pred. No. 7.2e-101;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 122 ASTKKGKSPVFLAPSSKSTSGTAAAGCLVXDYFPEPVTVSNWNGALTSVGHVTFPAVLQ 181
DB 1 AST--KGPSVFLAPCSRSTSESTAALGCLVXDYFPEPVTVSNWNGALTSVGHVTFPAVLQ 58
QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNKHKPNNTKVDKVEPKSCDKHTCTPCPAPELL 241
DB 59 SSGLYSLSSVTVTPSSSLGTQTYICNVNKHKPNNTKVDKVEPKSCDKHTCTPCPAPELL 115
QY 242 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQ 301
DB 116 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQ 175
QY 302 YNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
DB 175 FNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 235
QY 422 RWQGNVSCSVNHEALHNHYTKLSLSPGK 453
DB 296 RWQGNVSCSVNHEALHNHYTKLSLSPGK 327

RESULT 4
GC_RABIT
ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";

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Biochem. J. 116:249-259(1970).

[5]

SEQUENCE OF 129-131 AND 155-322.

Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Kallander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).

CC CC -1- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
markers and Ref.5 the E15 marker.

CC CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.

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CC CC -----

DR EMBL; M16426; AAA31289.1; -;
DR PIR; A91749; GHRB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; Ig LIKE; 3.
DR PROSITE; PS00290; Ig_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Repeat.
KW NON TER 1 1
FT DOMAIN 1 6 96 IG-LIKE 1.
ET DOMAIN 114 213 IG-LIKE 2.
ET DOMAIN 222 318 IG-LIKE 3.
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VP (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 50.6%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 8.4e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 127 KGPSVFPLAPSSKSTSGGTAALGLCLVLYDYFPEPVTWNSGALTSVGVHFFPAVLQSSGLY 186
DB 4 KAPSVFPLAPCGDTPSSVTTLGLCLVLYDYFPEPVTWNSGALTSVGVHFFPAVLQSSGLY 63

QY 187 SLSSVTVFSSSLGQTQVTCNVNHPKNTKVDKVEKSCDKHTCTCPAPPELLGGPSV 246
DB 64 SLSSVSVTSSS---QPTVCNVAHPATNTKVDKTVAPSTCCK---PTCPPELLGGPSV 116

QY 247 FLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAKTKPRREQYNSTY 306
DB 117 FLFPKPKDITLMISRTPEVTCVVDVSDDBEVQFTWYINNEQVTRTAPPLREQQFNSTI 176

QY 307 RVVSULTVHQDLNGKVEYCKVSNKALPAPIEKTISKAKGQPREPQVYITPPRREEMTK 366
DB 177 RVVSTLPIPHQDLNLRGKFKCKVHNKALPAPIEKTISKARGQPREPQVYITPPRREELSS 236

QY 367 NOVSLTCLVKGFPYSDTAIVWESNGQPNNTKTPPVLDSGDSFPLTSKLTVDKSRWQOG 426
DB 237 RSVSLTCTMINGFPYSDISVWEKQKAEADNYKTTTPAVLDSGDSYFLVKNKLSVPTSEWQRG 296

QY 427 NVFSCSVNMEALHNHYTKSLSPGK 453
DB 297 DVFTCSVNMEALHNHYTKSLSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DI 15-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K.; Huseain Q.Z.; Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J.; Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E.; Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M.; Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B.; Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: This chain was isolated from pooled serum of strain
13 inbred guinea pigs.
CC PIR; A94553; GZGP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; Ig LIKE; 3.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

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FT NON TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 50231B7164D1FBA9 CRC64;

Query Match 49.4%; Score 1202.5; DB 1; Length 329;
Best Local Similarity 69.2%; Pred. No. 9e-75;
Matches 231; Conservative 31; Mismatches 63; Indels 9; Gaps 4;

QY 123 STKGKGVFVPLAASSKSTSGTAAAGLVKVDYFPEPVTVVSNAGALTSCTGVHFFPAVLQS 182
Db 1 SARTAPSVFPLAASCVDTSGMMTLGCLVKGYPFPEPVTVKWSGALTSCTGVHFFPAVLQ- 59
QY 183 SGLYSLSVVTVPSSSLGTTQYICNVNHPKNTKVDKKVPKSCDKTH--TCPPCPAPEL 240
Db 60 SGLYSLSMTVPSQKAT---CNVAHPASSTKVDTVEIRTPZPBCTCPKCPPEN 115
QY 241 LGGSVFLFPKPKDITLISRTPTCVVDVSHEDPEVKNWYVDGVHNAKTPREE 300
Db 116 LGGSVFLFPKPKDITLISRTPTCVVDVSHEDPEVKNWYVDGVHNAKTPREE 175
QY 301 QYNSTYRVSVTLVHQDLNGKVKCKVSNKALPAPIETKTSKAGQPREPOVYTLPPS 360
Db 176 QYNSTYRVSVTLVHQDLNGKVKCKVSNKALPAPIETKTSKAGQPREPOVYTLPPS 235
QY 361 REETKNOVSLTCLVKGYPDSIAVEHNSQNP--ENNYKTPPVLSDSGFFLYSKLTV 418
Db 236 RDELKSKSVYTCIINFFPADIHVEWASNRVPVSEKEYKNTPTPIEDADGSYFLYSLTV 295
QY 419 DKSRWQQNVCSCVWHEALNHNHTQKSLSLSPG 452
Db 296 DKSAWDQGVTVTCVWHEALNHNHTQKSLSLSPG 329

RESULT 6
GC3_HUMAN
ID GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1988 (Rel. 01, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein WIS.";
RN [2]
RP Biochemistry 19:4304-4308(1980).
RX REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelisen T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.";
RN [3]
RP J. Biol. Chem. 252:883-889(1977).
RX REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RL Structure of the Fc fragment of immunoglobulin G3.";

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RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC interchain disulfide bond at position 7 in addition to the 11
CC normally present in the hinge region.
CC -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC Ref. 2.
CC -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC and all of the CH1 region.
CC -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC of the CH1 region, and part of the hinge compared with normal
CC gamma-3 heavy chains.
CC -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC or another gamma chain subclass.
CC -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC times as long as in other gamma chains and contains three
CC identical 15-residue segments preceded by a similar 17-residue
CC segment (12-28).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00231; AAA52805.1; ALT_SEQ.
DR HSSP; P01857; 1FCI.
DR Genew; HGNC:5527; IGHG3.
DR MIM; 147120; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Pyridolone carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.

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FT VARIANT 126 127 QV-> EB (IN ZUC).
FT VARIANT 134 134 /FTid=VAR_003890.
FT VARIANT 134 134 P-> L (IN OMM).
FT VARIANT 139 139 /FTid=VAR_003891.
FT VARIANT 139 139 F-> Y (IN OMM).
FT VARIANT 182 182 /FTid=VAR_003892.
FT VARIANT 182 182 T-> A (IN OMM).
FT VARIANT 227 227 /FTid=VAR_003893.
FT VARIANT 227 227 S-> N (IN OMM).
FT VARIANT 227 227 /FTid=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT VARIANT 279 279 /FTid=VAR_003895.
FT VARIANT 279 279 F-> Y (IN OMM).
FT VARIANT 279 279 /FTid=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CB9C95705B2F46 CRC64;

Query Match 47.8%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 3.9e-72;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 222 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 281
DB 59 EPKSCDTTPPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 118
QY 282 NRYVDGVVHNAKTPREEQNSTYRVSVLTVLHQQWLNKGYCKVSNKALPAPIEKT 341
DB 119 KXYVDGVVHNAKTPREEQNSTYRVSVLTVLHQQWLNKGYCKVSNKALPAPIEKT 178
QY 342 ISKAGQREQQVYTLPPSREEMTKNQVSLTCLVKGYFPEPSDIKAEVWESNGQENNYKTP 401
DB 179 ISKTKGQREQQVYTLPPSREEMTKNQVSLTCLVKGYFPEPSDIKAEVWESNGQENNYKTP 238
QY 402 PVLDSGDSGFFLYSKITVDKSRWQQNPFSCSVMEALHNHYTKSLSLSPGK 453
DB 239 PVLDSGDSGFFLYSKITVDKSRWQQNPFSCSVMEALHNHYTKSLSLSPGK 290

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RESULT 7
GC1_RAT ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7EAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003897; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF0047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; immunoglobulin C region; Glycoprotein.
FT NCN_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 245 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EP49B9DA CRC64;

Query Match 47.3%; Score 1150; DB 1; Length 326;
Best Local Similarity 64.0%; Pred. No. 3e-71;
Matches 210; Conservative 51; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVFPLAPSSKSTSGTAAALGCLVDPYFPEPTVWNSGALTSGVHTFPAVLQSSGLYSL 188
DB 6 PSVYPLAPGTALKSNMVTGLCLVKGYPPEPTVWNSGALTSGVHTFPAVLQ-SGLYTL 64
QY 189 SSVTVPSSSLGTQYICNVNHPKNTKVDKVEKSCDKTHTCPCPAPELGG---PS 245
DB 65 TSVTVPSSTWPSQTVCNVAHPASTKVDKIVPRNCG--GDCRKC----TCTSEVSS 118
QY 246 VLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFNNVYDGVVHNAKTPREEQYNST 305
DB 119 VFIFPPKPKDVLITILTPKVTCTVVDVDSQDDPEVHFSMFVDDVEVHTAQTREPEQFNST 178
QY 306 YRVSVSLTVLHQWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT 365
DB 179 FRSVSELPIHQDWLNGRTFRCKVTSAAFPSPTEKTSKPEGRQVPHVYTMSPTEEMT 238
QY 366 KQVSLTCLVKGYFPEPSDIKAEVWESNGQENNYKTPPVLDSGDSGFFLYSKITVDKSRWQQ 425
DB 239 QNEVSTICVKGYPFDIYVWQMGQPOENYKNTPTMTDTSYFLISKLVNKKKQWQ 298
QY 426 GNVFCSVMHEALHNHYTKSLSLSPGK 453
DB 299 GNTFTCSVLHLEGLHNHTKSLSHSPGK 326

RESULT 8
GC1_MOUSE ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T.; Obata M.; Yamawaki-Kataoka Y.; Kataoka T.; Kawakami T.;
RA Takahashi N.; Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]_
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M.; Yamawaki-Kataoka Y.; Takahashi N.; Kataoka T.; Shimizu A.;
RA Mano Y.; Seidman J.G.; Peterlin B.M.; Leder P.; Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]_
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J.; Clarke P.; Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]_
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).

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RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.; Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gamma1 chain.
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RA MEDLINE=73008889; PubMed=5073237;
RX Svasti J.; Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.;"
RL Biochem. J. 126:837-850(1972).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; GIMS.
DR GlycoSuiteDB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DSULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DSULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DSULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DSULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DSULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DSULFID 138 198
FT CARBOHYD 174 174
FT FTID=CAR_000055.
FT DSULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
FT SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
SQ
Query Match 47.0%; Score 1142; DB 1; Length 324;
Best Local Similarity 63.0%; Pred. No. 1e-70;
Matches 206; Conservative 54; Mismatches 10; Gaps 4;
QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSYIPLAPSAAGTNSMTLGLVKGYFPEPTVTVWNSGSLSSGVHTFPAVLQSD-LYTL 64
QY 189 SSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPD--CPAPELLGSPSV 246

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Db 65 SSVTVTPSSPRPSEITVTCNVAHPASSTKVDDKIVPRDCG----CKPCICTVPEV---SSV 117
QY 247 FLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKREEQYNSTY 306
Db 118 FIFPPKPKDVLITITLTKVTCVVVDISKDDPEVQSFVDDVEVHTAQTQPREEQFNSTF 177
QY 307 RVVSVTLVTLHQDLNKGKVKCKVSKNKAAPLPIETKTISKAKGQPREPQVYVTPPPSREEMTK 366
Db 178 RSVSELPIMHQDLNKGKFKCRVNSAAPPAPIETKISKTKGRPKAPQVYVTPPPKPEQMAK 237
QY 367 NQVSLTCLVKGYFPGSDIAVEWESNGQPENNYKTTPTPLDSDGSGFYSKYSLTVDKSRWQOG 426
Db 238 DKVSTCTMTDPFDITVEWQNGQPENYKNTQPIIMNTNGSYFVSKLNVQKSNWEAG 297
QY 427 NVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 298 NITFTCSVLEGLNHHHTEKLSLSHPGK 324
RESULT 9
GC3_MOUSE STANDARD; PRT; 329 AA.
ID GC3_MOUSE AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig Gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.;"
RL EMBL J. 3:2041-2046(1984).
CC
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CC
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
CC PIR; B02156; G3MSC.
CC HSP; P01857; IFC1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; Igc1; 2.
CC PROSITE; PS00835; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
SQ
Query Match 47.0%; Score 1142; DB 1; Length 329;
Best Local Similarity 65.1%; Pred. No. 1e-70;
Matches 213; Conservative 44; Mismatches 66; Indels 4; Gaps 3;
QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSSGLYSL 188

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Db 5 PSVPLVPGCDSTGSSVTLGCLVKGYPPEVTVKMNYSALSSGVRTVSSVLQ-SGFYSL 63
 QY 189 SSVTVPRSSSLGTQTYICNVNHPKSNKTKVDKVKPKSCDKHTCP--PCPAPELLGGPSV 246
 Db 64 SSVTVPRSSSLGTQTYICNVNHPKSNKTKVDKVKPKSCDKHTCP--PCPAPELLGGPSV 122
 QY 247 FLFPKPKDMLTMSPTPVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREEQYNSTY 306
 Db 123 FIFPKPKDMLTMSPTPVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREEQYNSTY 182
 QY 307 RVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREEMTK 366
 Db 183 RVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREEMTK 242
 QY 367 NOVSTCLVKGYPSPDIAVEHNSQPNNTKTPPVLDSGSPFLYSKLTVDKSRMQQG 426
 Db 243 KKVSLTCLVKNFSEAISEVNERNGELRQDYKNTKPPILDSGTYFLYSKLTVDKSRMQQG 302
 QY 427 NVFSCSVNHEALHNHYTKSLSPGK 453
 Db 303 EIFTCSVNHVHEALHNHYTKSLSPGK 329

RESULT 10

GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 DR PIR; PS0018; PS0018.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR001110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00847; ig. 3.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS00835; IG-LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 96 IG-LIKE 1.
 FT DOMAIN 124 223 IG-LIKE 2.
 FT DOMAIN 232 328 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 147 207
 FT DISULFID 253 311
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D4B40A6 CRC64;

Query Match 46.9%; Score 1139.5; DB 1; Length 333;
 Best Local Similarity 64.4%; Pred. No. 1.6e-70;
 Matches 213; Conservative 44; Mismatches 65; Indels 9; Gaps 3;

QY 129 PSVPLVPGCDSTGSSVTLGCLVKGYPPEVTVKMNYSALSSGVRTVSSVLQ-SGFYSL 188
 Db 6 PSVPLVPGCDSTGSSVTLGCLVKGYPPEVTVKMNYSALSSGVRTVSSVLQ-SGFYSL 64

QY 189 SSVTVPRSSSLGTQTYICNVNHPKSNKTKVDKVKPKSCDKHTCP--PCPAPELLGGPSV 246
 Db 65 TSSVT--SSTWPSQVTCNVAHPASSTKVDKVKERRNGIGHKCPTCTCHKCPVPELIG 122
 QY 243 GRSVFLFPKPKDMLTMSPTPVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREEQYNSTY 302
 Db 123 GPSVFIFPKPKDMLTMSPTPVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREEQYNSTY 182
 QY 303 NSTYRVSVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRE 362
 Db 183 NSTYRVSVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSRE 242
 QY 363 EMTKNOVSLTCLVKGYPSPDIAVEHNSQPNNTKTPPVLDSGSPFLYSKLTVDKSRMQQG 422
 Db 243 QLTEQVSVTCLTSGFLPNDIGVEMTSNGHIEKNYKNTPEVMDSDGSPFLYSKLTVDKSRMQQG 302
 QY 423 WQGNVFCVSVNHEALHNHYTKSLSPGK 453
 Db 303 WDSRAPFVCSVNHVHEALHNHYTKSLSPGK 333

RESULT 11

GCB_MOUSE ID GCB_MOUSE STANDARD; PRT; 393 AA.
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG gamma-1 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yanawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "cDNA for surface immunoglobulin gamma chains encodes a highly
 conserved transmembrane sequence and a 28-residue intracellular
 domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=External;
 CC Note=May be the major isoform;
 CC -----

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CC -----
 CC EMBL; V00793; CAA24172.1; -;
 CC EMBL; V00793; CAA24173.1; -;
 CC EMBL; V00793; CAA24174.1; -;
 CC PIR; B02159; G1MSM.
 CC PDB; 1SC8; 23-MAR-99.
 CC PDB; 1A86; 18-MAR-98.
 CC PDB; 1CL7; 12-JAN-00.
 CC PDB; 1F11; 06-FEB-01.
 CC PDB; 1F58; 29-DEC-99.
 CC PDB; 1KCS; 24-JUL-02.
 CC PDB; 1KCR; 11-MAY-02.
 CC PDB; 25C8; 09-JUL-99.
 CC MGD; MGI:96446; Igh-4.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_C1.
 CC InterPro; IPR003006; IG_MHC.
 CC Pfam; PF00047; Ig; 2.
 CC SMART; SM00407; IGc1; 2.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane; 3D-structure.
 CC -----
 CC NON_TER 1
 CC DOMAIN 1 97 CH1.
 CC DOMAIN 98 110 HINGE.
 CC DOMAIN 111 217 HINGE.
 CC DOMAIN 218 324 CH3.
 CC DISULFID 27 82
 CC DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 CC DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 138 138 N-LINKED (GLCNAC. .).
 CC CARBOHYD 174 174
 CC DISULFID 244 302
 CC TRANSMEM 340 357 POTENTIAL.
 CC DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
 CC SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 46.8%; Score 1137; DB 1; Length 393;
 Best Local Similarity 62.9%; Pred. No. 2.8e-70;
 Matches 205; Conservative 54; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
 DB 6 PSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD-LYTL 64
 QY 189 SSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCTCP--CPAPELLGGPSV 246
 DB 65 SSVVTPSSPRPSETVTCNVHPASSTKVDKIVPRDCG---CKPCICTVPEV---SSV 117
 QY 247 FLPPPKPDFTLMSRTEPTVCVVVDVSHEDPEVKFNWYVDGVEFNNAKTPKEBQVNSTY 306
 DB 118 FIPIPKPKVLTITLTPKTCVVVDISKDDPEVQFSWFDVDEVHTAQTQPEEFGNSTF 177
 QY 307 RVVSVLTFLHODMLNGEKYCKYSKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 366
 DB 178 RVSVELPIMEQDMLNGEKFKCRVNSAFAPIEKTISKYGRKAPQVVTIPPKQMAK 237
 QY 367 NOVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKRWQOG 426
 DB 238 DKVSLTCLMTIDFFPEDITVEWQNGQPAENYKNTQPIMTNNGSYFYFYSKLNQKSNWAG 297
 QY 427 NVFSCSYNEALHNHYTKSLSPG 452

DB 298 NTFTCSVLHGLHNHTTKSLSHSPG 323
 RESULT 12
 ID GC3M MOUSE STANDARD; PRT; 398 AA.
 AC P03987;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-3 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
 RN [2]
 RP SEQUENCE OF 328-398 FROM N.A.
 RX MEDLINE=84041483; PubMed=6314258;
 RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
 RA Wall R.;
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
 segment.";
 RL Nucleic Acids Res. 11:6775-6785(1983).
 CC -----
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CC -----
 CC EMBL; J00451; AAB59655.1; -;
 CC EMBL; V01526; CAA24767.1; ALT_SEQ.
 CC PIR; A02156; G3MSM.
 CC HSP; P01857; IFC1.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_C1.
 CC InterPro; IPR003006; IG_MHC.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00407; IGc1; 2.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 CC NON_TER 1 1
 CC DOMAIN 1 97 CH1.
 CC DOMAIN 98 113 HINGE.
 CC DOMAIN 114 223 CH2.
 CC DOMAIN 224 327 CH3.
 CC TRANSMEM 346 362 POTENTIAL.
 CC DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
 CC CONFLICT 333 333 E -> G (IN REF. 2).
 CC CONFLICT 342 342 E -> Q (IN REF. 2).
 CC CONFLICT 388 388 P -> F (IN REF. 2).
 CC SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 46.5%; Score 1131; DB 1; Length 398;
 Best Local Similarity 64.9%; Pred. No. 7.4e-70;
 Matches 211; Conservative 44; Mismatches 66; Indels 4; Gaps 3;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
 DB 5 PSVYPLPGCSDTSSSVTLGCLVKGYFPEPTVKMNYGALSSGVRTVSVLQ-SGFYSL 63
 QY 189 SSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCTCP--PCPAPELLGGPSV 246

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Db 64 SSVLVTPSTWPSQVVICNVAPASKTLIKRIER-IPKESTPGSCPCGNILGPSV 122
QY 247 FLPFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 306
Db 123 FLPFPKPKDMLMISLTPKVTCTVVVDVSEDDPDVHVSFWDNKEVHNTAWTPREARQYNSTF 182
QY 307 RVVSVLTVLHODWLNKGVKCKVSNKALPAPIETKTIISKAGQPREPOVYITLPPSRRENTK 366
Db 183 RVVSVLTVLHODWLNKGVKCKVSNKALPAPIETKTIISKAGQPREPOVYITLPPSRRENTK 242
QY 367 NOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGDSGFFLYSKLTVDKSRWQQG 426
Db 243 KKVSLTCLVNTFFSEISVEMERNGELQDYKNTPEILDSDGTFLYSLKLVDTSDMLQG 302
QY 427 NVFSCSVVHEALHNHYTKSLSP 451
Db 303 EFTCSVHVEALHNHHTTKNLSRSP 327

RESULT 13
GCAA_MOUSE
ID GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL Balb/c gamma 2a heavy chain messenger RNA.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=62627279;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RL and evolution of heavy chain genes: further evidence for intervening
RL sequence-mediated domain transfer.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RL family.";
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgeois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RL immunoglobulin: amino-acid sequence of the FC fragment. Implications
RL for the evolution of immunoglobulin structure and function.";
RN [5]
RP Eur. J. Biochem. 43:423-435(1974).
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RL immunoglobulin. Identification of the disulfide bridges.";
RN [6]
RP Eur. J. Biochem. 30:452-462(1972).
CC 1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PSS0835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B94361C5445A6864 CRC64;

Query Match 46.3%; Score 1126; DB 1; Length 330;
Best Local Similarity 64.0%; Pred. No. 1.3e-69;
Matches 212; Conservative 42; Mismatches 73; Indels 4; Gaps 3;

QY 125 KGKGPSVFPPLAPSSKSTSGTALGLVADYDPEPTVSVNSGALTSGVHTPEAVLQSSG 184
Db 2 KTTAPSVYPLAPVCGDTTSSVTGLCLVKGYPPEPTVLTWNSGSLSGSVHTFPVAVLQSD- 60
QY 185 LYSLSVSVTVPPSSSLGTQTVICNVNHPKNTKVDKVEPKSCDKTHTCPP--CPAPELIG 242
Db 61 LYLTLSSSVTVTSWPSQSITCNVAHPASSTKVDKXIEPRG-FTIKPCPCPCAPNLLG 119
QY 243 GPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 302
Db 120 GPSVFLFPKPKDMLMISLTPKVTCTVVVDVSEDDPDVHVSFWDNKEVHNTAWTPREARQY 179
QY 303 NSTRVVSVLTVLHODWLNKGVKCKVSNKALPAPIETKTIISKAGQPREPOVYITLPPSRRE 362
Db 180 NSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIETKTIISKAGQPREPOVYITLPPSR 239
QY 363 EMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGDSGFFLYSKLTVDKSR 422
Db 240 EMTKKQVTLTCMVTDPMPEDIYVEWTNGKTELNYKNTPEVLDSDGSGFYMSKLRVEKN 299
QY 423 WQCGNVFSCSVVHEALHNHYTKSLSPGK 453
Db 300 WVERNSYSCSVVHVEGLHNHHTTKSFRTPGK 330

RESULT 14
GCAAB_MOUSE
ID GCAAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Borhwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
IG22a and Igg2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
CC -I- SUBCELLULAR LOCATION: Secreted (Potential).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -I- MISCELLANEOUS: The sequence differs from that of the a allele,
from BALB/c mice, at 15% of the positions.
CC -I- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; ; NOT_ANNOTATED_CDS.
DR PIR; A02153; GZMSAB.
DR PDB; 1BOG; 23-MAR-99.
DR PDB; 1HH6; 26-JAN-01.
DR PDB; 1HH9; 24-JUL-03.
DR PDB; 1HI6; 08-FEB-01.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 46.2%; Score 1123.5; DB 1; Length 335;
Best Local Similarity 61.8%; Pred. No. 1.9e-69;
Matches 207; Conservative 51; Mismatches 70; Indels 7; Gaps 2;

QY 125 KKGPSVFPLAPSKSTSGGTAALGCLVVDYFPEPVTVSNNSGALTSGVHTFPVQLQSSG 184
Db 2 KTTAPSVYPLVPCVGGTGGSVTLGCLVKGYPFEPVTLTWNSSLSGVHTFPALLQ-SG 60

QY 185 LYSLSVVTVFSSSLGTQTVICNVHKNPSNTKVDKVEPK-----SCDKTHTCPCPAP 238
Db 61 LYLSSSVTVTSNTWPSQTTCNVHAPASSTKVDKIEPRVP;TQNPPHQRVPFPCAAP 120

QY 239 ELGCGPSVFLFPKPKDGLMISRTPEVT;CVVVDVSHEDPEVKFNWVVDGVHNAKTKR 298
Db 121 DLLGGPSVFFFPKIKDVLMSLSPMT;CVVVDVSEDDPDVQLSWFNWVNVHTAQTH 180

QY 299 EEQNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPRPQVYITLP 358
Db 181 REDYNSTLRVVSALPIQHODMSGKEFKCKVNNRALPSIEKTISKPRGVPAPQVYVLP 240

QY 359 PSSEETKNOVSLTCLVKGFPSPDIAVESNGOPENNYKTPPVLDSDGSPFLYSKLTIV 418
Db 241 PPAEMTKKEFSLTCLMTGFLPAEIAVDWTSNGRTEQNTATVLDSDGSPFYMSKLRV 300

QY 419 DKSRWQGNVFSVSMHEALHNHYTKSLSLSPGK 453
Db 301 QKSTWERSGLFAGSVVHEVLHNHLTKTISRSLGK 335

RESULT 15
GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=External;
CC Note=Probably the major isoform;
CC -I- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00471; AAB59661.1; ALT_INIT.
DR PIR; A02154; GZMSAM.
DR PDB; 1XB5; 08-APR-98.
DR PDB; 1YEE; 15-OCT-97.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing; 3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT CARBOHYD 180 180
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Query Match 46.1%; Score 1121; DB 1; Length 399;
Best Local Similarity 63.9%; Pred. No. 3.6e-69;
Matches 211; Conservative 42; Mismatches 73; Indels 4; Gaps 3;

QY 125 KGKGPSVPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 184
Db 2 KTTAPSVYPLAPVCGDITGSSVTIGCLVKGYFPEPVLTWNSGSLSSGVHTFPAVLQSD- 60
QY 185 LYSLSVVTVPSLSIGTQTYICNVNHPSTNTKDKVEPKSCDKTHTCPP-CPAPELLG 242
Db 61 LYTLLSSVTVTSSTWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPCCKCPAPNLLG 119
QY 243 GPSVFLRPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 302
Db 120 GPSVFIFPPPKIKDVLMSLSFIVTCVVVDVSEDDPDQISWFWNNVEVHTAQITQTHREDY 179
QY 303 NSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRE 362
Db 180 NSTLRVVSALPIQHQDWMGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEE 239
QY 363 EMTKNQVSLTCLVKGYFPEVDIAVWESNGOPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 422
Db 240 EMTKKQVTLTCMTDFEPEDIYVEWTNNGKTELNKNTPEVLDSDGSGYFMYSKLRVEKN 299
QY 423 WOQGNVFSCSYMHEALHNHYTQKSLSLSPG 452
Db 300 WVERNSYSCSVVHEGLNHNHTTKSFRTPG 329
```

Search completed: May 13, 2004, 15:45:56
Job time : 15.1773 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:36:43 ; Search time 48.608 Seconds
(without alignments)
2940.454 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVLVSGGGLVQGGSLRL.....MHEALHHYTKSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0., Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_muc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	2153	88.5	470	4	Q725W1	Q725w1 homo sapien
2	2115	87.0	482	4	Q72351	Q72351 homo sapien
3	2043.5	84.0	469	4	Q727P5	Q727P5 homo sapien
4	2019.5	83.0	521	4	Q8N4Y9	Q8N4Y9 homo sapien
5	1903	78.2	473	4	Q8TC63	Q8TC63 homo sapien
6	1611.5	66.3	509	4	Q8NF17	Q8NF17 homo sapien
7	1552.5	63.8	469	11	Q8R3V9	Q8R3V9 mus musculus
8	1530.5	62.9	354	4	Q85WT2	Q85WT2 homo sapien
9	1511.5	62.2	437	11	Q8RL14	Q8RL14 mus musculus
10	1469.5	60.4	463	11	Q99LC4	Q99LC4 mus musculus
11	1463.5	60.2	473	11	Q91Z05	Q91Z05 mus musculus
12	1458	60.0	470	11	Q7TMK1	Q7TMK1 mus musculus
13	1450.5	59.6	473	11	Q9D8L4	Q9D8L4 mus musculus
14	1424	58.6	468	11	Q99L11	Q99L11 mus musculus
15	1423.5	58.5	473	11	Q92L25	Q92L25 mus musculus
16	1371	56.4	474	11	Q8R3H6	Q8R3H6 mus musculus

ALIGNMENTS

RESULT 1

Q725W1 PRELIMINARY; PRT; 470 AA.

AC Q725W1; 2003 (TREMREL. 25, Created)

DT 01-OCT-2003 (TREMREL. 25, Last sequence update)

DE 01-OCT-2003 (TREMREL. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E., Jones S.U., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

SEQ	SEQUENCE	469 AA; 51395 MW; CQD5BE12BAAF795C CRG64;
	Query Match	84.0%; Score 2043.5; DB 4; Length 469;
	Best Local Similarity	85.5%; Pred. No. 4.7e-160;
	Matches 389; Conservative	25; Mismatches 34; Indels 7; Gaps 5;
QY	1	EVLVESGGGLVQPGSIRLSCAVSGYSITSGISWNIKIQAPCKGLEWASIT-YDGSTN 59
DB	20	QVHLVQSAGAEVKPKGASVKLGSKTSGGNFSS-YDLIIVQAQCQGLEWGWISAHNGDTK 78
QY	60	YADSVKGRFTISRDDSKNTFFYLWNLSLRADTAIVYCARGSHYFGH-WHFVAWGQGTLLVT 118
DB	79	YARKEFGVRWTMTDTSATTSYMEFRSLRSDTALFYCATKS--GQVGDFDSWGQGTLLVT 136
QY	119	VSSASTKGKGSVPFLAPLSSKSTSGGTAALGCLVKDYFPPEPTVTVSNSSALTSGVHTTPA 178
DB	137	VSSAST--KGPSVFPLPSSKSTSGGTAALGCLVKDYFPPEPTVTVSNSSALTSGVHTTPA 194
QY	179	VLIQSGGLYSLGSVTVTPSSSLGTQTYICNNNHKPSNTKYDKVEPKSCDKTHTCPCPCAP 238
DB	195	VLIQSGGLYSLGSVTVTPSSSLGTQTYICNNNHKPSNTKYDKVEPKSCDKTHTCPCPCAP 254
QY	239	ELLGGPSVFLPPPKQDTLMISRTPETVCVVVDVSHEDDEVFNKVTVGDGEVHNNAKTTPR 298
DB	255	ELLGGPSVFLPPPKQDTLMISRTPETVCVVVDVSHEDDEVFNKVTVGDGEVHNNAKTTPR 314
QY	299	BEOYNSTRVVSVLTVLHODWLNKYEKCCKVSNKALPAPIEKTISKAKGPPEPOVYTLP 358
DB	315	EQYINSTRVVSVLTVLHODWLNKYEKCCKVSNKALPAPIEKTISKAKGPPEPOVYTLP 374
QY	359	PSREEMTKNQVSLTCLVKGFYPSPDIADVESNQGPNENNYKTTTPPVLDSDGSFFLYSKLTV 418
DB	375	PSRDELTKNQVSLTCLVKGFYPSPDIADVESNQGPNENNYKTTTPPVLDSDGSFFLYSKLTV 434
QY	419	DKSRWQQGVNFSCSVMHREALHHYTKQSLSLSPGK 453
DB	435	DKSRWQQGVNFSCSVMHREALHHYTKQSLSLSPGK 469
RESULT	4	
Q8N4Y9	ID	Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC	Q8N4Y9	PRELIMINARY; PRT; 521 AA.
DT	01-OCT-2002	(TrEMBLrel. 22, Created)
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_Taxid	9606;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RP	TISSUE=Primary B-Cell;	
RA	Strausberg R.;	
RL	Submitted (JUN-2002) to the ENBL/GenBank/DBBJ databases.	
RL	EWEL; BC033178; AAB33178.1; -.	
DR	PIR; A60764; A60764.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003597; IG_c1.	
DR	InterPro; IPR003006; IG_MHC.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF00047; IG; 4.	
DR	SMART; SMC0407; IGc1; 3.	
DR	SMART; SMC0406; IGv; 1.	
DR	PROSITE; PS50835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; 2.	
KW	Hypothetical protein	
SEQ	SEQUENCE	521 AA; 57156 MW; 2ACTD22E72D6CAA2 CRC64;
	Query Match	83.0%; Score 2019.5; DB 4; Length 521;
	Best Local Similarity	77.2%; Pred. No. 5.2e-158;
	Matches 390; Conservative	23; Mismatches 37; Indels 55; Gaps 5;

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RESULT 5
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025985; AAR25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPRO000923; BlueCu 1.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO03596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 78.2%; Score 1903; DB 4; Length 473;
Best Local Similarity 80.4%; Pred. No. 1.9e-148;

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QY 175 TPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNTKVDKKVEPKSCDKHTCPP 234
DB 197 TPAVLQSD-LYTLSSSVTPSSSTWPSQTVCNVAHPASSTKVDKKIVPRDCG---CKP 251
QY 235 --CPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVN 292
DB 252 CICTVPEV---SSVFIFFPKPKDVLITLTPKVTCVVVDISKDDPEVQFSFVDDVEVHT 308
QY 293 AKTKPREQYNTYRVSVLTVLHODWLNKGKEYKCKVSNKALPAPIETKISKAKGQPREP 352
DB 309 AQTKPREQFNSTFRSVSELPIHQDLWLNKEFKCRVNSAFAFFAPIETKISKTKGRPKAP 368
QY 353 QYVTLPPSREEMTKNQVSLTCLVKGYFSPSDIAVEVESNGQPENNYKTTPVLDSGGSFFL 412
DB 369 QYVTLPPKPKQAKDKVSLCMTDFEFEDITVEQWNGQPAENYKNTQPLMDTDSGYFV 428
QY 413 YSKLTVDKSRWQGNVFCVSMVHEALHNHYTKSLSLSPGK 453
DB 429 YSKLVNQSKEAGNTFCVSLHLEGLHNHTEKSLSHSPGK 469

RESULT 8
Q86TT2 PRELIMINARY; PRT; 354 AA.
ID Q86TT2 AC Q86TT2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CSD01019F20 of placenta of Homo sapiens
  (Human) (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta.
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta.
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248278; CAD62606.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 354 AA; 39125 MW; 238808F4D2B87A92 CRC64;

Query Match 62.9%; Score 1530.5; DB 4; Length 354;
Best Local Similarity 81.9%; Pred. No. 6.7e-118;
Matches 290; Conservative 7; Mismatches 10; Indels 47; Gaps 1;

QY 147 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC 206
DB 1 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC 60
QY 207 NVNKPSTNKVDKKY----- 221
DB 61 NVNKPSTNKVDKRVELKLTPLGDTHTCPCEPKSCDTPPPCPCPEKSCDTPPPCPR 120
QY 222 --EPKSCDTHTCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV 279
DB 121 CPKPCSDTPPPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV 180

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RESULT 9

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Q9RI14 PRELIMINARY; PRT; 437 AA.
ID Q9RI14 AC Q9RI14;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gammal heavy chain of Mab7 (fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
  antibody (Mab 7, its light and heavy chains) and construction of a
  single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR PIR; B45837; B45837.
DR PDB; 1CQK; 11-SEP-99.
DR PDB; 1191; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;

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Query Match 62.2%; Score 1511.5; DB 11; Length 437;
 Best Local Similarity 62.1%; Pred. No. 3.3e-116;
 Matches 282; Conservative 70; Mismatches 83; Indels 19; Gaps 7;

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QY 2 VQLVESGGGLVQPQGSRLRLSCAVSGYSITSGYSVNWIRAPQKGLWVASITYDGSNTYA 61
DB 1 VQ-QESGGGLVQPGSLKLSCAASGFTFS-YAMSWVRQTPEKRLWVASFSGGLIYTT 59
QY 62 DSVKGFRTTIRDDSKNTFYIQNNSLRADTAVVYCARSGSHYFCHWHFAVWGQTLTVSS 121
DB 60 DSVKGFRTIYKDKRNLISLQMSLSRSEDATANYCARGD-----YSAYMGPTLTVSA 113
QY 122 ASTKGGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
DB 114 AKT--TPPSVYPLAPGSAAGTNSMTLGLVKGYPPEPVTVTWNSGSLSSGVTTPAVLQ 171
QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNNVHKPSNTKVDKKVEPKSCDKHTCPP--CPAPE 239
DB 172 SD-LYTLSSSVTVPSSTWPSSEITVCNVAHPASSTKVDKKIVPRDCG---CKEICTVPE 226
QY 240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 299

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Db 227 V---SSVFIPEPKPKDVTITLTIPKATCVVVDISKDDPEVQFSWFVDDVEVHTAQTPRE 283
QY 300 EQYNSTYAVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPP 359
Db 284 EQFNSTFSVSELPIHODWLNKGEFKCKRVNSAFAFPAPIEKTISKTKGRPKAPOVYITPP 343
QY 360 SREEMTKQVSLTCLVKGFPSDIAVESNGQPENNYKTPPPVLDSDGFFLYSKLTVD 419
Db 344 PQEQAQKVKSLTCTMITDFPEDITVEMQWQPAENYKNTQIPIMDTDGSYFVYSKLVQ 403
QY 420 KSRWQGNVFCSSVMHEALHNHYTKSLSLSPGK 453
Db 404 KSNWEAGNTFTCSVLHGLHNHTEKSLSHSPGK 437
RESULT 10
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -
DR PIR; B45837; B45837.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Igi; 3.
DR SMART; SM00406; Igi; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 60.4%; Score 1469.5; DB 11; Length 463;
Best Local Similarity 60.0%; Pred. No. 1.1e-112;
Matches 274; Conservative 77; Mismatches 89; Indels 17; Gaps 9;
QY 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSTN- 59
Db 20 QVQLQSGAELARPGASVRLSCASGYTFT-GYGVSWYKQRTGGQLEWVGEI-YPGSGNT 77
QY 60 -YADSVKGRFTISRDDSKNTFYLQNSLRAEATAVYICARGSHYFGHWHPAVWGQGLT 118
Db 78 YXSEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAVYFCARSS-YYSYDLFAVWGQGLT 136
QY 119 VSSASTKKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVYVYVSNWNSGALTSGVHTP 178
Db 137 VSAAKT--TPPSVYPLAPGSAQAQNSMTLGLLVKGYFPEPVYVYVSNWNSGALTSGVHTP 194
QY 179 VLQSGSLVSSVTVPPSSSLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPP--CP 236
Db 195 VLQSD-LYTLSSSVTVPPSSSTPSETVQNAHPASSSTKVDKIVPRDCG---CKPCLCT 249
QY 237 APPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGEVHNATK 296
Db 250 VFEV---SSVFIPEPKPKDVLITITTPKVTCTVVDVSDISKDDPEVQFSWFVDDVEVHTAQ 306
QY 297 PREEQYNSTYAVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYIT 356
Db 307 PREEQFNSTFSVSELPIMHODWLNKGEFKCKRVNSAFAFPAPIEKTISKTKGRPKAPOVYIT 366

QY 357 LPSPREMTKQVSLTCLVKGFPSDIAVESNGQPENNYKTPPPVLDSDGSPFLYSKL 416
Db 367 IFPPKEQKQAKDKVSCMTITDFPEDITVEMQWQPAENYKNTQIPIMDTDGSYFIYSKL 426
QY 417 TVDKSRWQGNVFCSSVMHEALHNHYTKSLSLSPGK 453
Db 427 NVQKSNWEAGNTFTCSVLHGLHNHTEKSLSHSPGK 463
RESULT 11
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; F-electron transporter activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR000345; Cytochrome_B5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Igi; 3.
DR SMART; SM00406; Igi; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
Query Match 60.2%; Score 1463.5; DB 11; Length 473;
Best Local Similarity 61.6%; Pred. No. 3.4e-112;
Matches 286; Conservative 62; Mismatches 95; Indels 21; Gaps 9;
QY 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSTN- 59
Db 20 EVLVESGGGLVQPGSLRLSCAASGFTF-SDYGMHWVRQAPEKLEWVAYIN-SGSTTI 77
QY 60 -YADSVKGRFTISRDDSKNTFYLQNSLRAEATAVYICARGSHYFGHW--HFAVWGQGL 116
Db 78 YVADTVKGRFTISRDNKNTLFLQMTLSRSEDAMYICAREL-----WLRDYGQGT 132
QY 117 VTSSASTKKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVYVYVSNWNSGALTSGVHT 176
Db 133 ITVSSAKT--TPPSVYPLAPGCGDITGSSVTLGCLVKGYFPEPVYVYVSNWNSGALTSGVHT 190
QY 177 PAVLQSGSLVSSVTVPPSSSLGTQYICNVNHPKNTKVDKVPKSCDKT-HTCPE- 234
Db 191 PALLO-SGYITWSSSVTVPPSSSTPSETVQNAHPASSSTKVDKVPKSCDKTHTCPPC 249
QY 235 -----CPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGE 289
Db 250 KECHKCPAPNLEGPSVFIPEPKPKDVLITITTPKVTCTVVDVSDISKDDPEVQFSWFV 309
QY 290 VHNATKPREEQYNSTYAVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQ 349
Db 310 VHTAQQTREDYNTYRVSALPIQHQDWMNGKFEKCKVNNKDLPSPTERTISKIKGLV 369
QY 350 REPOVYITLPPSREMTKQVSLTCLVKGFPSDIAVESNGQPENNYKTPPPVLDSDG 409
Db 370 RAPQVILPPAPQLSRKDVSLTCLVVGFPNGDISVEMTSNGHTEENYKDTAPVLDSDG 429

QY 410 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSISLSPGK 453
:
Db 430 YFLYSKLDIKTSKWEKTDSCNVRHGLKNLYLKTTISRSPGK 473

RESULT 12

Q7TWK1	PRELIMINARY;	PRT;	470 AA.
AC	Q7TWK1;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
DE	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_Taxid=10090;		
ON	[1]		
RE	SEQUENCE FROM N.A.		
RP	STRAIN=CZECH II; TISSUE=Breast tumor;		
RC	MEDLINE=22388257; PubMed=12477932;		
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarano P.H.,		
RA	Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Musny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		

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RP SEQUENCE FROM N.A.
RC STRAIN=CZECH 11; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; RAH55910.1; -.
KW Hypochemical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90B4DF86BB090 CRC64;

      Query Match          60.0%; Score 1458; DB 11; Length 470;
Best Local Similarity    60.3%; Pred. No. 9.6e-112;
Matches 275; Conservative 71; Mismatches 102; Indels 8; Gaps 6;

QY   1 EVQLVESGGGLVQPGRSLRLSCAVSGYSITSGYSWNWIRQAQKGLIEWASIT-YDGSTN 59
Db   20 EVQLQQSGPELVKPGASVKISCKASGVTF-T-GYYMHWKQSHGSKSLEWIGLVNPNGDTS 78
QY   60 YADSVKGSGFTSRDDSKATFLQNWSLRADETAVYICARGSHYFGHHHPAVWGQQTLLTV 119
Db   79 YNQKPKGKATLTVDKSSSTAYMELNSITSDSAVTTCARYTSGSYFEDVMGAGTTTIV 138
QY   120 SSASTKKGKPSVFPLAPRSKSTSGTAAALCLVKIDFPPPEPTVSWNSGALTISGVTFFPAV 179
Db   139 SAATT--TAPSIVFLVPCCGTSSGVTLCGLVKGFPPPEPTVKMNYGALSISGVATVSVV 196
QY   180 LQSSGLYSLSVVTPSPSSSLGTQTYICNVNHKFSNTKVDKKBPVKSCDKTHTCP--PGPA 237
Db   197 LQ-SGFYSLSLAVTPESSTWPSQIVICNAVHPASKTELICKIEPR-I PKSTFPQGSSCPP 254
QY   238 PELLGGPSVFLPFPKPDKTLMIISTPETHCVVDVDSHEDPEVKFNWYDVGVVEVHNATKP 297

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255	GNI	GGSPSVFIPPPKPKDALMISLTPKVT	CVVVDVDSDDPDVHVSVFVNDKEVHTIAWTQ	314
298	R	EQYNSTYRVVSVLTVLHWDLWNGKEYKCKVSKNALP	APIETKTSKAGQKQPREPQVYL	357
315	R	EQYNSTYRVVVSALPIQHQDMWKGKGFCKVKNNALP	APIETKTSKPKGRATPOVYTI	374
358	P	SRBEMTKNQVSLTCLYGYPISDIAVEWESNGQPENNY	KTTPPVLDSDSGSFFLYSKLT	417
375	P	PPPEQMGKKVYSUTCLVTNFFSAISVVEWIRGELE	QDYKNTPPILDSGTGYFLYSKLT	434
418	V	DKSRWQQQNFVSCSVMEALHNHYTKQISLSLSPGK	453	
435	V	ITDGLWLGEGEFTCSVYVHEALHNHGTOKNLSRSPGK	470	

RESULT 13

Q9D8L4	PRELIMINARY;	PRT;	473 AA.
ID	Q9D8L4		
AC	Q9D8L4;		
DT	01-JUN-2001	(T-EMBLrel. 17, Created)	
DT	01-JUN-2001	(T-EMBLrel. 17, Last sequence update)	
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)	
DE	1810060009Rik protein.		
GN	IGH-1 OR 1810060009RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		

RP SOURCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsueda Y., Nikaido I., Resole G., Quackenbush J.,
RA Schirrali L.M., Staubli F., Suzuki R., Tomita M., Wegner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maghina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";

Nature 407:695-690(2001).
DR EMBL; accession numbers: BAB25349.1; -.
DR PIR; S26746.
DR HSSP; P01842; 2FAB.
DR MGD; MGJ_96443; Igh-1.
DR InterPro; IPRO0110; Ig-like.
DR TrEMBL; IPR003006; IG_MHC.
DR InterPro; IPRO03596; ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IGC; 1.
DR PROSITE; PS00290; IGM;
SQ SEQUENCE 473 AA; 51699 MW;

Query Match	59.6%	Score 1450.5	DB 11	Length 473
Best Local Similarity	59.6%	Pred. No. 4e-111		
Matches 274	Conservative			
Matches 74	Mismatches 99			
	Indels 13			
	Gaps 7			

Qy 1 EVLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQA PKGLEWVASI -TYDGSIN 59
 :|||:||| |||:|||::||| ||| |||::|||::||| | |||
Db 20 OVLUKOSGAEVLVKPGASVKISCKASYTFD-YYINWKVRPQGQLEWGKGIGSGGSTY 78

```
QY 60 YADSVKGRFTISRDRSKNTFYLOMNSLRADTAIVYCARSGHYFGHMFHFWGQGLTVV 119
Db 79 YNEKFKGKATLTADKSSSTAYNQLSLTSEDSSAVYFCAR--SGYDYDM--FAYWGQGLTVV 136
QY 120 SSASTKKGPSVFLPLAPSSKSTSGGTAALGCLVCKDYFPEPTVSNWNGALTSVGHVTFPAV 179
Db 137 SAAKT--TAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAL 194
QY 180 LQSSGLYLSVSVVTPSSSLGTQTYICNVNHPKSNTKVDKVKPK-----SCDKTHTCP 233
Db 195 LQ--SGLYLTSSSVTTSNTWPSQTTICNVNHPASSTKVDKVKIEPRVPTQPCPPLKECP 253
QY 234 PCPAPELLGCGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 293
Db 254 PCAAPDLLGCGPSVFLPPPKIDVLMISLSPMTVCVVVDSEDDPDVQISFVNVEVHTA 313
QY 294 KTKPREQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKQPREPQ 353
Db 314 QQTREDYNSTRVVSALPIQHDWMSGKEFKCKVNNRALLPSPIETKISKPRGVRAPQ 373
QY 354 VYTLPPREEMTKNOVSLTCLVKGYFPSDIAVEWESNGOPENNYKTTTPVLDSDGSSEPLY 413
Db 374 VYVLPPEAEEMTKKFSLTCTMTGFLPAEIAVDWTSNGRTQNYKNATVLDSDGSIFMY 433
QY 414 SKLTVDKSRWQGNVFSVCSVMHEALHNHYTKQSLSPCK 453
Db 434 SKLRVQKSTWERSGLFACSVVHEGLNHLTKTISRSLGK 473

RESULT 14
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 58.6%; Score 1424; DB 11; Length 468;
Best Local Similarity 60.1%; Pred. No. 6.1e-109;
Matches 274; Conservative 64; Mismatches 108; Indels 10; Gaps 7;

QY 1 EVOLVESGGLVQPGSRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASI--TYDGSN 59
Db 20 EVQLQSQDAELVRPGASVKLSCTASGFIKDSL--MHWVKQRPEQGLEWIGIDPEDGETK 78
QY 60 YADSVKGRFTISRDRSKNTFYLOMNSLRADTAIVYCARSGHYFGHMFHFWGQGLTVV 119
Db 79 YAPKFDKATLTADTSNTAYLQLSLTSEDTAIYCARNLVGGYDY--WGQGLTVV 136
QY 120 SSASTKKGPSVFLPLAPSSKSTSGGTAALGCLVCKDYFPEPTVSNWNGALTSVGHVTFPAV 179
Db 137 SAAKT--TAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAL 194
QY 180 LQSSGLYLSVSVVTPSSSLGTCTICNVNHPKSNTKVDKVKPKSCDKTHTCP--CPA 237
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Db 195 LQSD--LYTLSSSVTVTSSTWPSQISICNVNHPASSTKVDKVKIEPRG--PTIKPCPPCKCPA 252
QY 238 PELLGCGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 297
Db 253 PNLGCGPSVFLPPPKIDVLMISLSPMTVCVVVDSEDDPDVQISFVNVEVLTQTQT 312
QY 298 REQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKQPREPQVYTL 357
Db 313 HREDYNSTRVVSALPIQHDWMSGKEFKCKVNNKALPAPIETKISKPKSVRAPQVYV 372
QY 358 PPSREEMTKNOVSLTCLVKGYFPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLT 417
Db 373 PPEEEMTKQVTLTCMTDFPEDIYVETWNNKTELNYKNTEPVLDSGSGYFMYSKLR 432
QY 418 VDKSRWQGNVFSVCSVMHEALHNHYTKQSLSPGK 453
Db 433 VEKKNVVERNSYSCSVVHEGLNHHHTKFSRTPGK 468

RESULT 15
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 58.5%; Score 1423.5; DB 11; Length 473;
Best Local Similarity 59.5%; Pred. No. 6.8e-109;
Matches 273; Conservative 72; Mismatches 103; Indels 11; Gaps 8;

QY 1 EVOLVESGGLVQPGSRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASI--TYDGSN 59
Db 20 QVQLQSQDAELVKPGASVKISKVSGYTFD--HTIHWVKQRPEQGLEWIGYIYPRDGTK 78
QY 60 YADSVKGRFTISRDRSKNTFYLOMNSLRADTAIVYCAR--GSHYFGH--WHFAVWGQGLT 116
Db 79 YNEKFKGKATLTADKSSSTAYNQLSLTSEDSSAVFCSSGSIYGYGYFYDYWGQGLT 138
QY 117 VTSSASTKKGPSVFLPLAPSSKSTSGGTAALGCLVCKDYFPEPTVSNWNGALTSVGHVTF 176
Db 139 ITVSSAKT--TAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTF 196
QY 177 PAVLQSSGLYLSVSVVTPSSSLGTQTYICNVNHPKSNTKVDKVKPKSCDKTHTCP-- 234
Db 197 PAVLQSD--IYTLSSSVTVTSSTWPSQISICNVNHPASSTKVDKVKIEPRG--PTIKPCPPCK 254
QY 235 CPAPELLGCGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 294
Db 255 CPAPELLGCGPSVFLPPPKIDVLMISLSPMTVCVVVDSEDDPDVQISFVNVEVLTQA 314
QY 295 TKPREEQYNSTRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKQPREPQ 354
```

Db 315 TQTHREDYNSTLRVVSALPIQHDMGSGKEFKCKVNNKALPAPIERTISKPGSVRAPQV 374
QY 355 YTLPPSRBEEMTKQVSLTCLVKGFYPSDIAVWESNGQFENNYKTPPEVLDSGGSFFLYS 414
Db 375 YVLPPEBEEMTKQVTLTCMTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSGGSFYFYS 434
QY 415 KLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
Db 435 KLRVEKKWVERNSYSCSVVHEGLNHHHTKSFSTRPCK 473

Search completed: May 13, 2004, 15:47:21
Job time : 50.608 secs

OM protein - protein search, using sw model
Run on: May 13, 2004, 15:08:53 ; Search time 32.8137 Seconds
(without alignments)
1877.123 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQTQPSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_28Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	100.0	218	AAW95658	Mus muscu
2	1135	100.0	218	AAW85300	Light cha
3	1135	100.0	218	AAW76947	Full vari
4	1128	99.4	218	AAW33312	Humanised
5	1112	98.0	218	AAW95660	Mus muscu
6	1112	98.0	218	AAW95662	Mus muscu
7	1112	98.0	218	AAW50030	Human E27
8	1112	98.0	218	AAW07472	Amino aci
9	1112	98.0	218	AAW74211	E27 anti-
10	1112	98.0	218	AAW62797	E27 anti-
11	1109	97.7	218	AAW95664	Mus muscu
12	1109	97.7	218	AAW95669	Mus muscu
13	1109	97.7	218	AAW47087	Anti-IgE
14	1109	97.7	218	AAW76949	Full leng
15	1109	97.7	218	AAW76951	Full leng
16	1109	97.7	218	AAW76953	Variable
17	1109	97.7	218	AAW76958	Variable
18	1108	97.6	218	AAW13563	Humanised
19	1100	96.9	238	AAW90930	Humanised
20	1100	96.9	238	AAW74899	Humanised
21	1099	96.8	238	AAW90932	Humanised
22	1099	96.8	238	AAW74901	Humanised
23	1096	96.6	238	AAW90931	Humanised
24	1096	96.6	238	AAW74900	Humanised
25	1036	91.3	214	AAW93735	The Kappa

ALIGNMENTS

RESULT 1

AAW95658
ID AAW95658 standard; protein; 218 AA.

XX AC AAW95658;
XX XX
DT 08-JUN-1999 (first entry)
XX XX
DE Mus musculus anti-IgE e25 full length variable light chain.
XX KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
XX KW histamine; production; hypersensitivity; allergen; anaphylaxis;
XX KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
XX KW eczema; anaphylactic shock; urticaria.
XX OS Mus musculus.
XX XX
PN WO9901556-A2.
XX XX
PD 14-JAN-1999.
XX XX
PF 30-JUN-1998; 98WO-US013410.
XX XX
PR 02-JUL-1997; 97US-00887352.
XX XX
PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI, 1999-106057/09.
XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
XX PT identifying aspartyl residues which undergo isomerisation and
XX PT substituting alternative residues and screening for affinity against the
XX PS target.
XX PS Disclosure; Page 91-92; 129pp; English.
XX CC The sequence is that of the full length variable light chain of e25. It
XX CC was used as part of a method to improve the affinity of anti-IgE
XX CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
XX CC for reducing or preventing IgE mediated production of histamine in a
XX CC mammal. They can be used for treating a disorder mediated by IgE such as
XX CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
XX CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
XX CC antibodies can also be used for affinity purification, detection and
XX CC diagnosis

SQ Sequence 218 AA;
Query Match 100.0%; Score 1135; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFFPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFFPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
AAY85200
ID AAY85200 standard; protein; 218 AA.
XX AC AAY85200;
XX 29-JUN-2000 (first entry)
XX DE Light chain amino acid sequence of the humanised MaE11 antibody.
XX KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCBL; PCEH;
XX KW low affinity binding receptor; high affinity binding receptor; allergy;
XX KW diagnosis; treatment; histamine release; light chain; prevent; chimeric.
XX OS Mus sp.
XX OS Homo sapiens.
XX PN US6037453-A.
XX PD 14-MAR-2000.
XX XX 06-JUN-1995; 95US-00466151.
XX PR 14-AUG-1992; 92WO-US008860.
XX PR 26-JAN-1994; 94US-00185899.
XX PR 15-MAR-1995; 95US-00405617.
XX XX (GETH) GENENTECH INC.
XX PI Presta LG, Jardieu PM;
XX DR WPI; 2000-269913/23.
XX XX New bispecific antibodies, useful for treating immunoglobulin E-mediated
XX PT disease, binds to IgE, but only when on the low affinity receptor, and to
XX PT an antigen other than IgE.
XX PS Claim 14; Fig 3; 48pp; English.

This sequence represents the light chain amino acid sequence of a
XX humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention
XX relates to a bispecific antibody that binds specifically to IgE when IgE
XX is bound to its low affinity receptor (FCBL), but does not bind to IgE,
XX when IgE is bound to its high affinity receptor (FCRH). The bispecific
XX antibody comprises an IgE-binding arm with human framework residues of a
XX recipient human antibody and donor murine CDR (complementarity
XX determining region) residues, but with at least one human CDR residue
XX replacing the analogous murine residue. The antibody also comprises an Fv
XX that is specific for a predetermined antigen other than IgE. The
XX antibodies work by displacing bound IgE from its receptor, or via

CC competitive inhibition of its binding. The bispecific antibodies are used
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated
CC diseases, also, when immobilised, for the isolation of FCBL from cells
CC (for research or therapy). The bispecific antibodies of the invention do
CC not cause granulation or release of histamine from mast cells
XX
SQ Sequence 218 AA;
Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFFPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFFPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 3
AAB76947
ID AAB76947 standard; protein; 218 AA.
XX AC AAB76947;
XX DT 17-APR-2001 (first entry)
XX DE Full variable light chain sequence of e25 SEQ ID 13.
XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX KW conjunctivitis; eczema; urticaria; food allergy.
XX OS Synthetic.
XX PN US6172213-B1.
XX PD 09-JAN-2001.
XX XX 30-JUN-1998; 98US-00109207.
XX PR 02-JUL-1997; 97US-0051554P.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 2001-122353/13.
XX XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX PT properties, produced by substituting aspartyl residues in unimproved
XX PT immunoglobulin E prone to isomerization by other residues by affinity
XX PT maturation with phage display.
XX XX Disclosure; Fig 2; 87pp; English.

This invention relates to a nucleotide sequence encoding an antibody with
XX improved anti-IgE antibody activity. The antibody has improved action due
XX to a process comprising, a) identifying aspartyl residues prone to
XX isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX substituting alternative residues to create candidate molecules, and c)
XX selecting those candidate molecules which display affinity against the
XX target molecule. Use of the antibody results in antiasthmatic;

CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
XX
SQ Sequence 218 AA;
Query Match 100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDGDSYNNWYQQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDGDSYNNWYQQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFLTITSLQPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDFLTITSLQPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
RESULT 4
AAR33312
ID AAR33312 standard; protein; 218 AA.
XX AC AAR33312;
XX DT 25-MAR-2003 (revised)
XX DT 05-JUL-1993 (first entry)
XX DE Humanised MaE11 Version 1 (intact IgG) light chain.
XX KW Antibody; high affinity; FCEH; low affinity; FCEI; IgE receptor;
KW histamine; mast cell; basophil; Kabat; CDR; murine; MaE11; Fab;
KW humael1v1.
XX OS Synthetic.
XX PN WO9304173-A1.
XX PD 04-MAR-1993.
XX PF 14-AUG-1992; 92WO-US006860.
XX PR 14-AUG-1991; 91US-00744768.
XX PR 07-MAY-1992; 92US-00879495.
XX PA (GETH) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 1993-094004/11.
XX PT Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE
PT antagonists; useful for treating and preventing IgE-mediated disorders
XX e.g. allergies.
XX PS Example 4; Fig 3; 113pp; English.
XX

CC Residues were selected from MaE11 and inserted or substituted into a
CC human Fab antibody background (Vh region Kabat subgroup III and VI region
CC kappa subgroup II). A first version, humael1v1 or version 1 is given
CC below. The affinity of version 1 was assayed and found to be ca. 100
CC times lower than that of the donor antibody MaE11. Therefore, further
CC modifications in the sequence of version 1 were made. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX
SQ Sequence 218 AA;
Query Match 99.4%; Score 1128; DB 2; Length 218;
Best Local Similarity 99.5%; Pred. No. 1.8e-56;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDGDSYNNWYQQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDGDSYNNWYQQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFLTITSLQPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDFLTITSLQPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
RESULT 5
AAR95660
ID AAR95660 standard; protein; 218 AA.
XX AC AAR95660;
XX DT 08-JUN-1999 (first entry)
XX DE Mus musculus anti-IgE e26 full length light chain.
XX KW Light chain; IgG; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.
XX OS Mus musculus.
XX PN WO9901556-A2.
XX PD 14-JAN-1999.
XX PF 30-JUN-1998; 98WO-US013410.
XX PR 02-JUL-1997; 97US-00887352.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 1993-106057/09.
XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX PS Disclosure; Page 94-95; 129pp; English.
XX CC The sequence is that of the full length light chain of e26. It was used
CC as part of a method to improve the affinity of anti-IgE antibodies such
CC as e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be

CC used for treating a disorder mediated by IGE such as hypersensitivity,
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
 CC for affinity purification, detection and diagnosis
 XX
 SQ Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 2; Length 218;
 Best Local Similarity 98.2%; Pred. No. 1.4e-55;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGSDYMMWYQKPKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGSDYMMWYQKPKAPKLLIYAASYLE 60
 QY 61 GVPSPFSGSGGSDTFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPSPFSGSGGSDTFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IFFPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQSDKSTYSL 180
 Db 121 IFFPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQSDKSTYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
 AAW95662
 ID AAW95662 standard; protein; 218 AA.
 AC AAW95662;
 XX
 DT 08-JUN-1999 (first entry)
 DE Mus musculus anti-IgE e27 full length light chain.
 KW Variable light chain; IGE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria.
 XX
 OS Mus musculus.
 XX
 PN WO9901556-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US013410.
 XX
 PR 02-JUL-1997; 97US-00887352.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 1999-106057/09.
 XX

Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.
 XX
 PS Disclosure; Page 97; 129pp; English.
 XX
 CC The sequence is that of the full length heavy chain of e27. It was used
 CC as part of a method to improve the affinity of anti-IgE antibodies such
 CC as e26 and e27. The e26 and e27 antibodies can be used for reducing or
 CC preventing IGE mediated production of histamine in a mammal. They can be
 CC used for treating a disorder mediated by IGE such as hypersensitivity,
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used

CC for affinity purification, detection and diagnosis
 XX
 SQ Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 2; Length 218;
 Best Local Similarity 98.2%; Pred. No. 1.4e-55;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGSDYMMWYQKPKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDVVTITCRASQSDVDGSDYMMWYQKPKAPKLLIYAASYLE 60
 QY 61 GVPSPFSGSGGSDTFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPSPFSGSGGSDTFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IFFPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQSDKSTYSL 180
 Db 121 IFFPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQSDKSTYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
 AAY50030
 ID AAY50030 standard; protein; 218 AA.
 AC AAY50030;
 XX
 DT 19-JAN-2000 (first entry)
 DE Human E27 anti-IgE antibody light chain.
 KW Immunoglobulin E; IGE; antibody; vascular endothelial growth factor;
 KW VEGF; chimeric; IGE; assay; Fc gamma receptor; low affinity; hexamer;
 KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
 KW light chain.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9951642-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US006858.
 XX
 PR 02-APR-1998; 98US-00054255.
 PR 15-JAN-1999; 99US-0116100P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Idusogie EE, Mulkerrin MG, Presta LG, Shields RL;
 XX
 DR WPI; 1999-620197/53.
 XX

Antibody variants useful in receptor binding assays and in therapy of
 PT conditions needing treatment.
 XX
 PS Example 1; Fig 4A; 69pp; English.
 XX
 CC This sequence represents human E27 anti-IgE (immunoglobulin E) antibody
 CC light chain, which, along with the E27 heavy chain (AAY50031), comprises
 CC the E27 anti-IgE antibody. The E27 antibody binds the constant regions of
 CC IGE, and when mixed with IGE in an equimolar ratio, forms a stable
 CC hexamer consisting of three E27 molecules and 3 IGE molecules. This
 CC complex-forming ability can be utilised in an assay for the binding of
 CC IGE to Fc gamma receptors Fc-gamma-1a, Fc-gamma-1b and Fc-gamma-1ii,
 CC which have IGE affinities in the micromolar range and so cannot be
 CC assayed via a standard ELISA (enzyme-linked immunosorbent assay)
 CC protocol. The low affinity receptor binding assay uses E27 and a

CC recombinant chimeric form of IgE, consisting of a human IgE Fc region and
CC the Fab regions of an anti-VEGF (vascular endothelial growth factor)
CC antibody, which binds two VEGF molecules per mole of anti-VEGF chimeric
CC IGE. When recombinant human VEGF is added at 2:1 molar ratio to the
CC IGE:E27 hexamer complexes, the hexamers are linked into larger complexes
CC via IGE Fab:VEGF interactions. The E27 component of this complex binds to
CC the Fc-gamma-IIIa, Fc-gamma-IIb and Fc-gamma-III alpha subunits to permit
CC detection via ELISA
XX
SQ Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 2; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-55;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDTLTITISSLOPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDTLTITISSLOPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8
AAB07472
ID AAB07472 standard; protein; 218 AA.
AC AAB07472;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of E27 and anti-IgE antibody light chain.
XX
KW anti-IgE antibody; light chain; Fc region; effector function; cancer;
KW allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
XX
OS Synthetic.
XX
PN WO200042072-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US000973.
XX
PR 15-JAN-1999; 99US-0116023P.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG;
XX
DR WPI; 2000-476035/41.
XX
PT New Fc region-containing polypeptides that have altered effector function
PT due to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX
PS Disclosure; Fig 4A; 132pp; English.
XX
CC The present sequence represents the E27 and anti-IgE antibody light
CC chain. The protein is used to produce Fc region-containing polypeptides
CC that have altered effector function as a consequence of one or more amino
CC acid modifications in the Fc region. The variant polypeptides are useful
CC for treating cancer, allergic conditions such as asthma (with an anti-IgE
CC antibody), and LFA-1-mediated disorders. Where the polypeptide binds the

CC HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a
CC benign or malignant tumour characterized by overexpression of the HER2
CC receptor. Such cancers include breast cancer, squamous cell cancer, small
CC -cell lung cancer, non-small cell lung cancer, gastrointestinal cancer,
CC pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder
CC cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma,
CC salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer,
CC vulval cancer, thyroid cancer, hepatic carcinoma and various types of
CC head and neck cancer
XX
SQ Sequence 218 AA;

Query Match 98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-55;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDTLTITISSLOPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDTLTITISSLOPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9
AAB74211
ID AAB74211 standard; protein; 218 AA.
AC AAB74211;
XX
DT 17-MAY-2001 (first entry)
XX
DE E27 anti-IgE antibody light chain.
XX
KW Antibody; antigen; cancer; allergy; asthma; LFA-mediated; autoimmune;
KW vasculitis.
XX
OS Unidentified.
XX
PN US6194551-B1.
XX
PD 27-FEB-2001.
XX
PF 31-MAR-1999; 99US-00282505.
XX
PR 02-APR-1998; 98US-0080447P.
XX
PA (GETH) GENENTECH INC.
XX
PI Idusogie EE, Presta LG, Mulkerrin MG;
XX
DR WPI; 2001-217935/22.
XX
PT Novel polypeptide variant useful for treating cancers, allergic diseases
PT such as asthma and autoimmune diseases, comprises human immunoglobulin-G
PT Fc region, retains the ability to bind antigen and does not activate
PT complement.
XX
PS Disclosure; Fig 4; 30pp; English.
XX
CC The present invention relates to a variant of an antibody having a human
CC immunoglobulin (Ig)G Fc region, with an amino acid substitution. The
CC mutant retains the ability to bind antigen. The invention is useful for
CC determining the presence of a protein of interest, by exposing the sample

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CC suspected of containing the protein to the antibody and determining the
CC binding of it to the sample. The antibody is also useful for treating
CC cancer, allergic conditions including asthma, LFA-mediated disorders,
CC autoimmune disorders and vasculitis
XX
SQ Sequence 218 AA;

Query Match          98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-55;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGSDSYNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGSDYNNWYQQKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGGTDFTLLISSLQPEDPATYYCQOSHEDPVTFCGQTKVEIKETVAAPSVF 120
Db 61 GVPSRFGSGSGGTDFTLLISSLQPEDPATYYCQOSHEDPVTFCGQTKVEIKETVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVWCLLNFPYREAKVQWVDNALQSGNSQESVTEQDSKDSYLS 180
Db 121 IFPPSDEQLKSGTASVWCLLNFPYREAKVQWVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
ABU62797
ABU62797 standard; protein; 218 AA.
XX
AC ABU62797;
XX
DT 11-SEP-2003 (first entry)
XX
DE E27 anti-immunoglobulin E antibody light chain.
XX
KW Antibody; human immunoglobulin G; autoimmune disorder; E27;
KW anti-immunoglobulin E.
XX
OS Synthetic.
XX
PN US6538124-B1.
XX
PD 25-MAR-2003.
XX
PF 03-OCT-2000; 2000US-00680145.
XX
PR 02-APR-1998; 98US-0080447P.
PR 31-MAR-1999; 99US-00282505.
XX
PA (GETH ) GENENTECH INC.
XX
XX Idusogie EE, Presta LG, Mulkerrin MG;
XX WPI; 2003-531086/50.
XX
XX New nucleic acid encodes an antibody variant that binds antigen or an
XX immunoadhesin variant that binds a ligand or receptor, useful for
XX preparing a composition for treating a disorder e.g., autoimmune
XX disorder.
XX
XX Example 1; Fig 4A; 30pp; English.
XX
XX The invention relates to a new isolated nucleic acid that encodes an
XX antibody variant that binds antigen or an immunoadhesin variant that
XX binds a ligand or receptor. The antibody or immunoadhesin variant
XX comprises a human immunoglobulin G C region. The nucleic acid is useful
XX for preparing a composition for treating a disorder e.g., autoimmune
XX disorder. The present sequence represents the amino acid sequence of the
XX E27 anti-immunoglobulin E antibody light chain
XX

```

Query Match 97.7%; Score 1109; DB 2; Length 218;
 Best Local Similarity 97.7%; Pred. No. 2.1e-55;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQOKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQOKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTGKVEIKRTVAAPSVF 120
 DB 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTGKVEIKRTVAAPSVF 120
 QY 121 IPPPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 DB 121 IPPPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
 AAW95669
 ID AAW95669 standard; protein; 218 AA.
 AC AAW95669;
 DT 08-JUN-1999 (first entry)
 DE Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2 fragment.
 KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; F(ab)'2 fragment.
 OS Mus musculus.
 PN WO9901556-A2.
 PD 14-JAN-1999.
 PF 30-JUN-1998; 98WO-US013410.
 PR 02-JUL-1997; 97US-00887352.
 PA (GETH) GENENTECH INC.
 PI Lowman HB, Presta IG, Jardieu PM, Lowe J;
 DR WPI; 1999-106057/09.
 XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.
 XX Disclosure; Page 104; 129pp; English.
 XX The sequence is that of the variable light chain F(ab)'2 fragment of e26
 CC and e27. It was used as part of a method to improve the affinity of anti-
 CC IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be
 CC used for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis
 XX Sequence 218 AA;
 SQ

Query Match 97.7%; Score 1109; DB 2; Length 218;
 Best Local Similarity 97.7%; Pred. No. 2.1e-55;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQOKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGSDYNNWYQOKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTGKVEIKRTVAAPSVF 120
 DB 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTGKVEIKRTVAAPSVF 120
 QY 121 IPPPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 DB 121 IPPPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13
 AAB47087
 ID AAB47087 standard; protein; 218 AA.
 XX AAB47087;
 AC AAB47087;
 DT 11-SEP-2003 (revised)
 DT 03-MAY-2001 (first entry)
 XX Anti-IgE antibody, E26, light chain.
 DE Light chain; heavy chain; anti-IgE antibody; E26; transfection;
 KW green fluorescent protein; GFP; promoter; expression.
 XX Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX WO200104306-A1.
 PN 18-JAN-2001.
 PD 11-JUL-2000; 2000WO-US018841.
 PF 12-JUL-1999; 99US-0143360P.
 PR (GETH) GENENTECH INC.
 PA Chisholm V, Crowley CW, Krummen LA, Meng YG;
 PI WPI; 2001-138352/14.
 DR Novel polynucleotide construct for screening and obtaining cells
 XX expressing high levels of desired protein, comprises amplifiable
 PT selectable gene, fluorescent protein gene and sequence encoding desired
 PT product.
 XX Disclosure; Fig 13A; 75pp; English.
 XX The sequences given in AAB47087-88 represent the light and heavy chains
 CC of the anti-IgE antibody, E26. These sequences were expressed by the
 CC construct of the invention, which comprises an amplifiable selectable
 CC gene, a green fluorescent protein gene (GFP), and a selected sequence
 CC encoding a desired product, which is operably linked to either the
 CC amplifiable selectable gene or to the GFP gene, and to a promoter.
 CC Constructs such as this, are useful for producing a desired product by
 CC introduction into a suitable eukaryotic cell, culturing the resultant
 CC eukaryotic cell under conditions so as to express the desired product,
 CC and recovering the desired product from the culture medium. The
 CC constructs are efficient for identifying and selecting for stable
 CC eukaryotic cells expressing high levels of a desired product. They are
 CC suitable for earlier and faster screening of transfected cells. (Updated
 CC on 11-SEP-2003 to standardise OS field)
 XX

SQ Sequence 218 AA;
 Query Match 97.7%; Score 1109; DB 4; Length 218;
 Best Local Similarity 97.7%; Pred. No. 2.1e-55;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSYVDYDGSYNNWYQKPKGAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTTITCRASKPVDGSDSYLNWYQKPKGAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQTKVEIKETVAAPSVF 120
 DB 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQTKVEIKETVAAPSVF 120
 QY 121 IFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 180
 DB 121 IFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 180
 QY 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14
 AAB76949 ID AAB76949 standard; protein; 218 AA.
 AC AAB76949;
 XX
 DT 17-APR-2001 (first entry)
 DE Full length light chain sequence of e26 SEQ ID 15.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-00109207.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 PS New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phase display.
 XX
 Claim 2; Fig 12; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules, and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antiinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest

CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 SQ Sequence 218 AA;
 Query Match 97.7%; Score 1109; DB 4; Length 218;
 Best Local Similarity 97.7%; Pred. No. 2.1e-55;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSYVDYDGSYNNWYQKPKGAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDRTTITCRASKPVDGSDSYLNWYQKPKGAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQTKVEIKETVAAPSVF 120
 DB 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQTKVEIKETVAAPSVF 120
 QY 121 IFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 180
 DB 121 IFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 180
 QY 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
 DB 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15
 AAB76951 ID AAB76951 standard; protein; 218 AA.
 AC AAB76951;
 XX
 DT 17-APR-2001 (first entry)
 DE Full length light chain sequence of e27 SEQ ID 17.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-00109207.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 PS New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phase display.
 XX
 Claim 4; Fig 12; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules, and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;

CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IGE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
SQ Sequence 218 AA;

Query Match 97.7%; Score 1109; DB 4; Length 218;
Best Local Similarity 97.7%; Pred. No. 2.1e-55;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDVVTITCRASQSDYDGSYNNWYQCKGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDVVTITCRASQSDYDGSYNNWYQCKGKAPKLLIYAASYLE 60
Qy 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
Db 121 IFPPSDEQLKGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
Qy 181 STLTLKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:45:26
Job time : 33.8137 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:38 ; Search time 10.7213 Seconds
(without alignments)
1049.728 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFRNGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	100.0	218	2	US-08-887-352B-13
2	1135	100.0	218	3	US-08-466-151-9
3	1135	100.0	218	3	US-09-109-207C-13
4	1135	100.0	218	3	US-09-296-005-13
5	1135	100.0	218	4	US-08-466-163B-9
6	1135	100.0	218	4	US-09-920-171-13
7	1135	100.0	218	4	US-09-802-096-9
8	1112	98.0	218	3	US-09-282-505-1
9	1112	98.0	218	3	US-09-054-255-1
10	1112	98.0	218	4	US-09-282-845-1
11	1112	98.0	218	4	US-09-680-145-1
12	1109	97.7	218	2	US-08-887-352B-15
13	1109	97.7	218	2	US-08-887-352B-17
14	1109	97.7	218	2	US-08-887-352B-19
15	1109	97.7	218	2	US-08-887-352B-24
16	1109	97.7	218	3	US-09-109-207C-15
17	1109	97.7	218	3	US-09-109-207C-17
18	1109	97.7	218	3	US-09-109-207C-19
19	1109	97.7	218	3	US-09-109-207C-24
20	1109	97.7	218	3	US-09-296-005-15
21	1109	97.7	218	3	US-09-296-005-17
22	1109	97.7	218	3	US-09-296-005-19
23	1109	97.7	218	3	US-09-296-005-24
24	1109	97.7	218	4	US-09-920-171-15
25	1109	97.7	218	4	US-09-920-171-17
26	1109	97.7	218	4	US-09-920-171-19
27	1109	97.7	218	4	US-09-920-171-24

Sequence 2, Appl1
Sequence 71, Appl1
Sequence 39, Appl1
Sequence 39, Appl1
Sequence 39, Appl1
Sequence 40, Appl1
Sequence 11, Appl1
Sequence 40, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 40, Appl1
Sequence 25, Appl1
Sequence 25, Appl1
Sequence 25, Appl1
Sequence 25, Appl1
Sequence 25, Appl1
Sequence 6, Appl1

28 1108 97.6 218 5 PCT-US96-13152-2
29 1036 91.3 214 4 US-09-472-087-71
30 1021 90.0 214 2 US-07-934-373C-39
31 1021 90.0 214 3 US-08-437-642B-39
32 1021 90.0 214 5 PCT-US93-07832-39
33 1016 89.5 214 2 US-07-934-373C-40
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35 1016 89.5 214 3 US-08-437-642B-40
36 1016 89.5 214 3 US-09-097-171A-2
37 1016 89.5 214 4 US-09-460-587-2
38 1016 89.5 214 5 PCT-US93-07832-40
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42 1016 89.5 214 4 US-09-705-686-25
43 1016 89.5 214 3 PCT-US93-07832-25
44 1016 89.5 214 3 PCT-US93-07832-25
45 1016 89.5 214 3 PCT-US93-07832-25

ALIGNMENTS

RESULT 1

US-08-887-352B-13
Sequence 13, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Prestra, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
IMPROVING POLYPEPTIDES
TITLE OF INVENTION: 26
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear

US-08-887-352B-13

Query Match 100.0%; Score 1135; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.7e-86;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQTQSPSSLSASVGRVTITCRASQVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60

Db 1 DIQTQSPSSLSASVGRVTITCRASQVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60

QY 61 GVPFRSGSGSGTDTLTITISLQPEDPATYICQSHEDPVTFGGTKEIKRTVAAPSVF 120

Db 61 GVPFRSGSGSGTDTLTITISLQPEDPATYICQSHEDPVTFGGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2

US-08-466-151-9
; Sequence 9, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svcboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-466-151-9

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSLSASVGDRTVITICRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSLSASVGDRTVITICRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDTLTITSSLOPEDFATYVCOQSHEDPYTFQGQTKVEIKRTVAAPSV 120

DB 61 GVPSRFSGSGGTDTLTITSSLOPEDFATYVCOQSHEDPYTFQGQTKVEIKRTVAAPSV 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 3

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRI
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITICRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSLSASVGDRTVITICRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDTLTITSSLOPEDFATYVCOQSHEDPYTFQGQTKVEIKRTVAAPSV 120
DB 61 GVPSRFSGSGGTDTLTITSSLOPEDFATYVCOQSHEDPYTFQGQTKVEIKRTVAAPSV 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1x
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRI
; ORGANISM: Artificial
; FEATURE:

; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-236-005-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60
DB 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60

QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 5
US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466.163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-08-466-163B-9

Query Match 100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60
DB 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60

QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 6

US-09-920-171-13
; Sequence 13, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-13

Query Match 100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60
DB 1 DIQLTQSPSSLSASVGDRTTTCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASVLES 60

QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 7

US-09-802-096-9
; Sequence 9, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-09-802-096-9

Query Match      100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9
US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6242195
US-09-282-846-1

Query Match      98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
US-09-282-846-1
; Sequence 1, Application US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-1

Query Match      98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
DB 61 GVPSPFSGSGSGTDFLTITISLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
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Db 121 IFFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
US-09-680-145-1
; Sequence 1, Application US/09680145
; Patent No. 6538124
; GENERAL INFORMATION:
; APPLICANT: Esche Kinaduese Iduscgie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/09/680,145
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6538124
US-09-680-145-1

Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDVVTITCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVGDVVTITCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGGTDFTLTISSLOPEDFATYICQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTISSLOPEDFATYICQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IFFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-08-897-352B-15
; Sequence 15, Application US/08897352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 2.4e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDVVTITCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVGDVVTITCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPFSGSGGTDFTLTISSLOPEDFATYICQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTISSLOPEDFATYICQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IFFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

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Best Local Similarity 97.7%; Pred. No. 2.4e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120

QY 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
Db 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match          97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 2.4e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120

QY 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
Db 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match          97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 2.4e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKETVAAPSVF 120

QY 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
Db 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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us-09-925-179-9.ra1

Thu May 13 16:10:51 2004

Search completed: May 13, 2004, 15:48:48
Job time : 11.7213 secs

16	1109	97.7	218	14	US-10-113-996-24	Sequence 24, Appl
17	1108	97.6	218	9	US-09-917-410-2	Sequence 2, Appl1
18	1100	96.9	238	14	US-10-216-484-127	Sequence 127, App
19	1100	96.9	238	14	US-10-384-933-127	Sequence 127, App
20	1099	96.8	238	14	US-10-216-484-131	Sequence 131, App
21	1099	96.8	238	14	US-10-384-933-131	Sequence 131, App
22	1096	96.6	238	14	US-10-216-484-129	Sequence 129, App
23	1096	96.6	238	14	US-10-384-933-129	Sequence 129, App
24	1036	91.3	214	14	US-10-153-382-19	Sequence 19, Appl
25	1036	91.3	238	14	US-10-216-484-107	Sequence 107, App
26	1036	91.3	238	14	US-10-384-933-107	Sequence 107, App
27	1031	90.8	238	14	US-10-216-484-50	Sequence 50, Appl
28	1031	90.8	238	14	US-10-384-933-50	Sequence 50, Appl
29	1028	90.6	218	15	US-10-449-566-98	Sequence 98, Appl
30	1028	90.4	260	15	US-10-264-049-2296	Sequence 2296, Ap
31	1020	89.9	214	15	US-10-449-566-102	Sequence 102, App
32	1019	89.8	214	15	US-10-423-299-3	Sequence 3, Appl1
33	1019	89.8	218	14	US-10-171-452A-39	Sequence 39, Appl
34	1019	89.8	218	14	US-10-171-452A-57	Sequence 57, Appl
35	1019	89.8	218	15	US-10-353-708-39	Sequence 39, Appl
36	1019	89.8	218	15	US-10-353-708-57	Sequence 57, Appl
37	1019	89.8	238	14	US-10-171-452A-38	Sequence 38, Appl
38	1019	89.8	238	14	US-10-171-452A-56	Sequence 56, Appl
39	1019	89.8	238	15	US-10-353-708-38	Sequence 38, Appl
40	1019	89.8	238	15	US-10-353-708-56	Sequence 56, Appl
41	1018	89.7	238	14	US-10-216-484-52	Sequence 52, Appl
42	1018	89.7	238	14	US-10-384-933-52	Sequence 52, Appl
43	1017	89.6	238	15	US-10-449-566-119	Sequence 119, App
44	1017	89.6	238	14	US-10-216-484-109	Sequence 109, App
45	1017	89.6	238	14	US-10-384-933-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-802-077-9
; Sequence 9, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/195,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-09-802-077-9

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Best Local Similarity	100.0%	Pred. No. 9e-64;		
Matches 218;	Conservative	0;	Mismatches	0;
			Indels	0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:47:29 ; Search time 25.3413 Seconds
(without alignments)
2393.762 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues
Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pcp.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	100.0	218	9	US-09-802-077-9
2	1135	100.0	218	9	US-09-802-096-9
3	1135	100.0	218	9	US-09-920-171-13
4	1135	100.0	218	10	US-09-925-179-9
5	1135	100.0	218	14	US-10-113-996-13
6	1120	98.7	218	10	US-09-925-179-67
7	1112	98.0	218	10	US-09-792-938-1
8	1112	98.0	218	14	US-10-292-869-1
9	1109	97.7	218	9	US-09-920-171-15
10	1109	97.7	218	9	US-09-920-171-17
11	1109	97.7	218	9	US-09-920-171-19
12	1109	97.7	218	9	US-09-920-171-24
13	1109	97.7	218	14	US-10-113-996-15
14	1109	97.7	218	14	US-10-113-996-17
15	1109	97.7	218	14	US-10-113-996-19

QY 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
US-09-802-096-9
; Sequence 9, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain
US-09-802-096-9

Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLOSPSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQLOSPSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLES 60
QY 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 3
US-09-920-171-13
; Sequence 13, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John

; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAEL1
US-09-920-171-13

Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLOSPSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQLOSPSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLES 60
QY 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFQGTKEIKRTVAAPSVF 120
QY 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IPPPDEQLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180
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RESULT 4
US-09-925-179-9
; Sequence 9, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain
US-09-925-179-9

Query Match 100.0%; Score 1135; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASVLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASVLES 60
QY 61 GVPFRFSGSGSDFTLTITSSLOPEDFATYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
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Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSVLS 180
QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218
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RESULT 5

US-10-113-996-13
; Sequence 13, Application US/10113996
; Publication No. US20030149244A1

GENERAL INFORMATION:

; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11

US-10-113-996-13

Query Match 100.0%; Score 1135; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSVLS 180
QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-09-925-179-67
; Sequence 67, Application US/09925179
; Publication No. US20030044858A1

GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)

; FILE REFERENCE: P0718P2C1D1CIUS

; CURRENT APPLICATION NUMBER: US/09/925,179

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 67

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Full-length light chain sequence corresponding to F(ab)9 of Tabl
US-09-925-179-67

Query Match 98.7%; Score 1120; DB 10; Length 218;
Best Local Similarity 97.7%; Pred. No. 7.8e-63;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASVLES 60

Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSTYNNWYQKPGKAPKLLIYAASVLES 60

QY 61 GVPFRFSGSGSDFTLTITSSLOPEDFATYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120

Db 61 GVPFRFSGSGSDFTLTITSSLOPEDFATYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSVLS 180

Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSVLS 180

QY 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7

US-09-792-938-1

; Sequence 1, Application US/09792938

; Publication No. US20030166869A1

; GENERAL INFORMATION:

; APPLICANT: Esche, Ekinaduse Idusogie et al.

; TITLE OF INVENTION: Polypeptide Variants

; FILE REFERENCE: P1266R1

; CURRENT APPLICATION NUMBER: US/09/792,938

; CURRENT FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 09/282,505

; PRIOR FILING DATE: 1999-03-31

; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 1

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: Artificial Sequence

; LOCATION: 1-218

; OTHER INFORMATION: Sequence is completely synthesized

US-09-792-938-1

Query Match 98.0%; Score 1112; DB 10; Length 218;
Best Local Similarity 98.2%; Pred. No. 2.5e-62;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 Db 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8

US-10-292-869-1
 ; Sequence 1, Application US/10292869
 ; Publication No. US20030158389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Esche Ekinaduse Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R2
 ; CURRENT APPLICATION NUMBER: US/10/292,869
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: US/09/282,846
 ; PRIOR FILING DATE: 1999-03-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 1
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-218
 ; OTHER INFORMATION: Sequence is completely synthesized
 US-10-292-869-1

Query Match 98.0%; Score 1112; DB 14; Length 218;
 Best Local Similarity 98.2%; Pred. No. 2.5e-62;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 Db 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9

US-09-920-171-15
 ; Sequence 15, Application US/09920171
 ; Patent No. US20020054878A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lowman, Henry B.
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Lowe, John
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
 ; FILE REFERENCE: P1123C2US

; CURRENT APPLICATION NUMBER: US/09/920,171
 ; CURRENT FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: US 08/887,352
 ; PRIOR FILING DATE: 1997-07-02
 ; PRIOR APPLICATION NUMBER: US 09/296,005
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 15
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-920-171-15

Query Match 97.7%; Score 1109; DB 9; Length 218;
 Best Local Similarity 97.7%; Pred. No. 3.8e-62;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 Db 121 IFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
 Db 181 STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10

US-09-920-171-17
 ; Sequence 17, Application US/09920171
 ; Patent No. US20020054878A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lowman, Henry B.
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Lowe, John
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
 ; FILE REFERENCE: P1123C2US
 ; CURRENT APPLICATION NUMBER: US/09/920,171
 ; CURRENT FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: US 08/887,352
 ; PRIOR FILING DATE: 1997-07-02
 ; PRIOR APPLICATION NUMBER: US 09/296,005
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 17
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-920-171-17

Query Match 97.7%; Score 1109; DB 9; Length 218;
 Best Local Similarity 97.7%; Pred. No. 3.8e-62;
 Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITICRASQSDVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 Db 61 GVPFRFSGSGGTDFTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy	121	IPPPDEQLKSGTASVWCLLNFFPRRAKQVQWKVDNALQSGNSQESVTEQDSKDSYSL	180
Db	121	IPPPDEQLKSGTASVWCLLNFFPRRAKQVQWKVDNALQSGNSQESVTEQDSKDSYSL	180
Qy	181	STLTLSKADYKHKHYACEVTHQGLSGPVTKSNRGE	218
Db	181	STLTLSKADYKHKHYACEVTHQGLSGPVTKSNRGE	218

```

RESULT 11
US-09-920-171-19
; Sequence 19, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: F1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-920-171-19

```

	Query Match	97.7%	Score 1109;	DB 9;	Length 218;
	Best Local Similarity	97.7%	Pred No. 3.8e-62;		
	Matches 21;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	DIQUTQPSLSASVGRDVITTCBASQSDYDGDSDYNNWTCQKCGKAPKLLIYAASVLS	60		
Db	1	DIQUTQPSLSASVGRDVITTCASRPDGDSDYLNWYQCKGKAPKLLIYAASVLS	60		
Qy	61	GVPSRFGSGSGTFTLTISLQBEDFATYYCQOSHEDPYTFGGTKVIEIKRTVAASVVF	120		
Db	61	GVPSRFGSGSGTFTLTISLQBEDFATYYCQOSHEDPYTFGGTKVIEIKRTVAASVVF	120		
Qy	121	IFPPSDQLKSGTASVVCLLNNFYFREAKQVMKDNALQSGNSQESVTEQDSKDSVLS	180		
Db	121	IFPPSDQLKSGTASVVCLLNNFYFREAKQVMKDNALQSGNSQESVTEQDSKDSVLS	180		
Qy	181	STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	218		
Db	181	STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	218		

```

US-10-113-996-15
  Order Information: Eight chain sequence derived from
  Query Match          97.7%; Score 1109; DB 14; Length 218;
  Best Local Similarity 97.7%; Pred. No. 3.8e-62;
  Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQTQSPSSLASVGDRVTITCRASQSDVDYDGBSYNNWYQQKPGKAPKLLIIAASYLE 60
Db 1 DIQTQSPSSLASVGDRVTITCRASKPVDGEGSYLNWYQQKPGKAPKLLIIAASYLE 60

Qy 61 GVPSRFGSGSGDTFTLTISLQPEFATYCCQSHEDPYTFQGQTKVEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGDTFTLTISLQPEFATYCCQSHEDPYTFQGQTKVEIKRTVAAPSVF 120

Qy 121 IFFPSDQLKSGTASVVCLLNPPYFREAKVQVDNALQSGNSQESVTEQDSKDSTYSLS 180

```

121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
DB 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:56:57
Job time : 26.3413 secs

121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
DB 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:56:57
Job time : 26.3413 secs

121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
DB 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:56:57
Job time : 26.3413 secs

121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
DB 61 GVPSRFGSGSGTDFLTITSSIQPEDFATYYCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:56:57
Job time : 26.3413 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:23 ; Search time 9.09687 seconds
(without alignments)
2305.161 Million cell updates/sec

Title: US-09-925-179-9

Perfect score: 1135

Sequence: 1 DIQLTQSPSLASVGDRTV.....EVTHQGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	942.5	83.0	215	2 JE0242	Ig kappa chain NIG
2	917.5	80.8	215	2 JE0244	Ig kappa chain NIG
3	892.5	78.6	215	2 JE0243	Ig kappa chain NIG
4	883	77.8	216	2 JE0241	Ig kappa chain Am3
5	875.5	77.1	215	2 A23746	Ig kappa chain V-I
6	759	66.9	240	2 S05084	Ig kappa chain pre
7	739	65.1	218	2 S69241	Ig kappa chain V r
8	727	64.3	218	2 JC5810	monoclonal antibody
9	727	64.1	230	2 S33161	Ig kappa chain - s
10	723	63.7	220	2 A31790	Ig kappa chain V r
11	718	63.3	234	2 S14237	Ig kappa chain pre
12	716	63.1	234	2 S01320	Ig kappa chain pre
13	712	62.7	210	2 A56169	Ig kappa chain V r
14	699	61.6	214	2 S68212	Ig kappa chain (Ma
15	698.5	61.5	219	2 S38665	Ig kappa chain - m
16	694.5	61.2	217	2 S42772	Ig kappa chain - m
17	693.5	61.1	225	2 S37484	Ig kappa chain - m
18	692.5	61.0	219	2 PC4203	Ig kappa chain (mo
19	689.5	60.7	219	2 S52028	Ig kappa chain - m
20	687.5	60.6	235	2 S25058	Ig kappa chain - m
21	683.5	60.2	219	2 S16112	Ig kappa chain V r
22	670.5	59.1	225	2 JL0029	Ig kappa chain pre
23	608	53.6	135	2 S52059	JC-kappa protein -
24	596	52.5	178	2 PT0219	Ig kappa chain V-C
25	563.5	49.6	229	2 A20969	Ig kappa chain pre
26	548	48.3	106	1 K3HU	Ig kappa chain C r
27	535.5	47.2	197	2 S29593	Ig kappa chain (WM
28	534.5	47.1	238	2 A49633	Ig lambda-like cha
29	513	45.2	99	2 A37927	Ig kappa chain C r

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 942.5; DB 2; Length 215;

Best Local Similarity 83.5%; Pred. No. 1.4e-55;

Matches 182; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

Qy 1 DIQLTQSPSLASVGDRTVITCRASQSDYDGDSDNNVYQKPGKAPKLLIYAASVLS 60

Db 1 EIVLTQSPGTLSPGERATLSCRASQSV---SNNYLAWYQKPGQAPSLIYDASSRAT 57

Qy 61 GVPSRFSGSGSDFTLTITSSLOPEDFATVYCOQSHEDPVTFQGTKEIKRTVAAPSVF 120

Db 58 GIPDRFSGSGSDFTLTITSSLOPEDFATVYCOQSHEDPVTFQGTKEIKRTVAAPSVF 117

Qy 121 IFPPSDQLKSGTASVYVCLNNFYPREAKVQKVDNALSGNSQESVTEQDSKDYSL 180

Db 118 IFPPSDQLKSGTASVYVCLNNFYPREAKVQKVDNALSGNSQESVTEQDSKDYSL 177

Qy 181 STLTLSKADYKHKVACEVTHQGLSPVTKSFNRGEC 218

Db 178 STLTLSKADYKHKVACEVTHQGLSPVTKSFNRGEC 215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL am

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

```
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 917.5; DB 2; Length 215;
Best Local Similarity 82.6%; Pred. No. 6.2e-54;
Matches 181; Conservative 14; Mismatches 19; Indels 5; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EVLVTQSPATLSVSPGERATLSCRASQSV----HSNLAWYQKPGQAPRLLIYRASTRAT 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GVPFRFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 GIPARFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 120 FIFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 FIFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 180 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
JE0243
IG kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      78.6%; Score 892.5; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 2.8e-52;
Matches 178; Conservative 16; Mismatches 20; Indels 5; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSV----ATNVVWYQKPGQAPRLLIYDASTRAT 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GVPFRFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 GVPARFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 120 FIFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 FIFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 180 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
JE0241
IG kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

```
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match      77.8%; Score 883; DB 2; Length 216;
Best Local Similarity 79.4%; Pred. No. 1.2e-51;
Matches 173; Conservative 17; Mismatches 26; Indels 2; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 DIVLTQSPDFLAIVSGERATINCKSSQSVLNKRNFLAWYQKPGQ-PKLLIW-ANVRES 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GVPFRFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 GVPDRFRGSGVGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 IFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 IFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
A23746
IG kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunog
C:Keywords: heterotrimer; immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match      77.1%; Score 875.5; DB 2; Length 215;
Best Local Similarity 81.1%; Pred. No. 3.7e-51;
Matches 176; Conservative 13; Mismatches 25; Indels 3; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYNNWYQKPGKAPKLLIYAASYLE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EIVLTQSPATLSVSPGERATLSCRASQSV----SSNYLAWYQKPGQAPRLLIYDASSRAT 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 GVPFRFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 GIPDRFSGSGGTDFTLTISSQLQPEDFATYVCCQSHEDPVTFCQGTKEIKRTVAAPSV 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 IFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 IFPPSDQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
S06084
IG kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cdn
A:Reference number: S06084; MUID:9001688; PMID:2508067
A:Accession: S06084
```


A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 66.9%; Score 759; DB 2; Length 240;
Best Local Similarity 65.5%; Pred. No. 2e-43;
Matches 144; Conservative 29; Mismatches 45; Indels 2; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDYDGD--SYNNWYQKPGKAPKLLIYAASYL 58
Db 21 DFVMTQSPSSLSASVAGETVTINCKSSQSLFYSGNKNYLAWYQKPGQSPKLLIYWASTR 80
Qy 59 EGVSRFRSGSGGDTFTLTISLQPEDPATYVCOQSHEDPVTGQGTVEIKRTVAAPS 118
Db 81 QGVGDFRFGSGSGGDTFTLTISVQAEALAIYCLQYETPTFGAGTKLEKRAAAPT 140
Qy 119 VFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 178
Db 141 VSIFFPSTEQATGASVCLNNFYPRDISVKMIDGTERDGLVDSVTQDSKSTYS 200
Qy 179 LSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218
Db 201 MSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRNEC 240

RESULT 7
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:G473962; PIDN:BAA06141.1; PID:G473963
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.
PES Lett 375, 273-275, 1995
A:Title: Thermolabile peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'NI', 3-212 <TAW>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 65.1%; Score 739; DB 2; Length 218;
Best Local Similarity 63.8%; Pred. No. 3.9e-42;
Matches 139; Conservative 30; Mismatches 49; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDYDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQAPKLLISLATNLES 60
Qy 61 GVPFRSGSGGDTFTLTISLQPEDPATYVCOQSHEDPVTGQGTVEIKRTVAAPS 120
Db 61 GVPFRSGSGGDTFTLTINHPVEEDVATYVCOHRELPLTFGAGTKLEKRAAAPT 120
Qy 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 180
Db 121 IFPPSDEQLTSGGASVCLNNFYPRDISVKMIDGTERDGLVDSVTQDSKSTYS 180

Qy 181 STLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218

RESULT 8
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
A:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dobmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphy
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a por
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 737; DB 2; Length 218;
Best Local Similarity 64.2%; Pred. No. 5.3e-42;
Matches 140; Conservative 28; Mismatches 50; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDYDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQAPKLLISLATNLES 60
Qy 61 GVPFRSGSGGDTFTLTISLQPEDPATYVCOQSHEDPVTGQGTVEIKRTVAAPS 120
Db 61 GVPFRSGSGGDTFTLTINHPVEEDVATYVCOHRELPLTFGAGTKLEKRAAAPT 120
Qy 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 180
Db 121 IFPPSDEQLTSGGASVCLNNFYPRDISVKMIDGTERDGLVDSVTQDSKSTYS 180
Qy 181 STLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHOGLSPVTKSFNRNEC 218

RESULT 9
S33161
Ig kappa chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
A:Accession: S33161
R:Foley, R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A:Description: Isolation and characterisation of sheep kappa light chain cDNA.
A:Reference number: S33161
A:Accession: S33161
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-230 <FOL>
A:Cross-references: EMBL:X54110; NID:G297103; PIDN:CAA38046.1; PID:G136421
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 727; DB 2; Length 230;
Best Local Similarity 63.8%; Pred. No. 2.6e-41;
Matches 139; Conservative 32; Mismatches 43; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDYDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 17 DIQVLTQSPSSLSASLTERVITCTTSQSV---SNLYNNWYQKPGQAPKLLIYATRLHT 72
Qy 61 GVPFRSGSGGDTFTLTISLQPEDPATYVCOQSHEDPVTGQGTVEIKRTVAAPS 120
Db 73 DVPSRFRSGSGGDTFTLTISNLEANDTATYCYESTPLAFGGGTNVEIKRSDAQPSVF 132

Query Match 64.1%; Score 727; DB 2; Length 230;
Best Local Similarity 63.8%; Pred. No. 2.6e-41;
Matches 139; Conservative 32; Mismatches 43; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDYDGDSYNNWYQKPGKAPKLLIYAASYLE 60
Db 17 DIQVLTQSPSSLSASLTERVITCTTSQSV---SNLYNNWYQKPGQAPKLLIYATRLHT 72
Qy 61 GVPFRSGSGGDTFTLTISLQPEDPATYVCOQSHEDPVTGQGTVEIKRTVAAPS 120
Db 73 DVPSRFRSGSGGDTFTLTISNLEANDTATYCYESTPLAFGGGTNVEIKRSDAQPSVF 132

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QY 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 133 LFKPSEELRGTRGVSVCLVNDFTPKQINVKVKGVDGVTQNSFNQSTDDQSKKSTYSL 192
QY 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
DB 193 STLTLSSEYQSHNAYACEVSHKSLPTALVKSFNKEC 230

RESULT 10
A31790
IG kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PID:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.7%; Score 723; DB 2; Length 220;
Best Local Similarity 61.4%; Pred. No. 4.5e-41;
Matches 135; Conservative 34; Mismatches 49; Indels 2; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDG--DSYMNWYQKPGKAPKLLIYAASYL 58
DB 1 DIWMTQSPSSLTVTAGEKVTMCTQSGLFNSGKQKNTLWYQKPGPPKVLIVASTR 60

QY 59 ESGVPSRFSGSGSDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTVAAPS 118
DB 61 ESGVPSRFSGSGSDFTLTISVQAEDLAVYCYQNDYSNPLTFGGGKLEKLRADAAPT 120

QY 119 VFIPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 178
DB 121 VFIPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

QY 179 LSSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
DB 181 MSSTLTLTQDEYERHNSYTCETHKTSPIVKSFNKEC 220

RESULT 11
S14237
IG kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R:Vandamme, A.M.; Bults, F.; Bernat, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody c
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBL:X56394; NID:G51622; PID:CAA39805.1; PID:G51623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 718; DB 2; Length 234;
Best Local Similarity 61.5%; Pred. No. 1e-40;
Matches 134; Conservative 35; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYMNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYMNWYQKPGKAPKLLIYAASYLE 60

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DB 21 DIKMTQSPSSMYASLGSRVTVTKASQDI---NSYLSWIQQKPGSKPTLIYRGNRLVA 76
QY 61 GYPSRFSGSGSDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTVAAPSVF 120
DB 77 GYPSRFSGSGSDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTVAAPSVF 136
QY 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 137 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 196

QY 181 STLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
DB 197 STLTLTQDEYERHNSYTCETHKTSPIVKSFNKEC 234

RESULT 12
S01320
IG kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, P.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DEI>
A:Cross-references: EMBL:X13187; NID:G51784; PID:CAA31579.1; PID:G51785
C:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <NAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 63.1%; Score 716; DB 2; Length 234;
Best Local Similarity 61.4%; Pred. No. 1.4e-40;
Matches 135; Conservative 33; Mismatches 44; Indels 8; Gaps 2;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDVDGDSYMNWYQKPGKAPKLLIYAASYL 58
DB 21 DIQMTQSPASLSVSGESVTITCRASENI-----YSNLAWYQKPGKAPKLLIYVATKL 74

QY 59 ESGVPSRFSGSGSDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTVAAPS 118
DB 75 VDGVPSPRFSGSGSDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTVAAPS 134

QY 119 VFIPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 178
DB 135 VSIFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 194

QY 179 LSSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 218
DB 195 MSSTLTLTQDEYERHNSYTCETHKTSPIVKSFNKEC 234

RESULT 13
A56169
IG kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R:Monfardini, C.; Kieber-Emmons, T.; Von Feldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godil
J. Biol. Chem. 270, 6628-6638, 1995
A:Title: Recombinant antibodies in bioactive peptide design.
A:Reference number: A56169; MUID:95204454; PMID:7896802
A:Accession: A56169
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-210 <MON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

```

Query Match 62.7%; Score 712; DB 2; Length 210;
Best Local Similarity 64.6%; Pred. No. 2.3e-40;
Matches 135; Conservative 28; Mismatches 46; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIVLTQSPASITVSLGQRTATISCRASKSVSSGYSHWYQKPGQPKVLIYIASNLES 60

QY 61 GVPFRFSGSGGTDFTLTITISLQPEDFATYVCOQSHEDPYTFGOGTKVEIKRTVAAPSVF 120
DB 61 GVPFRFSGSGGTDFTLTINHEVEREDAATYVCOHSRELPTWTFGGGTLEIKRADAAPTVS 120

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 121 IFPPSDEQLKSGTASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSL 180

QY 181 STLTLSKADYEKKHYACEVTHQGLSPV 209
DB 181 STLTLSKADYEKKHYACEVTHQGLSPV 209

RESULT 14
S38812
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 61.6%; Score 699; DB 2; Length 214;
Best Local Similarity 61.7%; Pred. No. 1.7e-39;
Matches 132; Conservative 34; Mismatches 46; Indels 2; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSV--DYDGDSDYNNWYQKPGKAPKLLIYAASYL 58
DB 1 DIVMTQSPSSLSASVGGQVTKSCSSQSLNSRNQKYLAWYQKPGQPKVLIYFPASTR 60

QY 59 ESGVPRFSGSGGTDFTLTITISLQPEDFATYVCOQSHEDPYTFGOGTKVEIKRTVAAPS 118
DB 61 ESGVPRFSGSGGTDFTLTISTVQAEADLADYFCQGHVSTPTTFGGGTLEIKRADAAPT 120

QY 119 VFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 178
DB 121 VSIFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSL 180

QY 179 LSSLTLSKADYEKKHYACEVTHQGLSPVTKS 212
DB 181 MSSLTLSKADYEKKHYACEVTHQGLSPVTKS 214

RESULT 15
S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R: Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 61.5%; Score 698.5; DB 2; Length 219;
Best Local Similarity 60.3%; Pred. No. 1.9e-39;
Matches 132; Conservative 34; Mismatches 52; Indels 1; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQS--VDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 59
DB 1 ELVMTQSPPLSVSLGDAQASISCRSSQSLVHTNGNTYLHWYQKPGKPLIYIVSNRF 60

QY 60 SGVPRFSGSGGTDFTLTITISLQPEDFATYVCOQSHEDPYTFGOGTKVEIKRTVAAPSV 119
DB 61 SGVPRFSGSGGTDFTLTISVREADLGVPFCSTVTPVTFGGGTLEIKRADAAPT 120

QY 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 179
DB 121 SIFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSL 180

QY 180 SSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218
DB 181 SSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 219

Search completed: May 13, 2004, 15:48:02
Job time: 10.0969 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:10:58 ; Search time 6.82265 Seconds
(without alignments)
1663.765 Million cell updates/sec

Title: US-09-925-179-9

Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	48.3	106	1 KAC_HUMAN	P01834 homo sapien
2	471	41.5	108	1 KVIH_HUMAN	P01600 homo sapien
3	467	41.1	111	1 KV3M_MOUSE	P01665 mus musculus
4	463	40.8	108	1 KVIH_HUMAN	P01597 homo sapien
5	462	40.7	111	1 KV3O_MOUSE	P01666 mus musculus
6	460	40.5	111	1 KV3N_MOUSE	P04431 homo sapien
7	460	40.5	129	1 KVIW_HUMAN	P01669 mus musculus
8	459	40.4	111	1 KV3Q_MOUSE	P01664 mus musculus
9	455	40.1	111	1 KV3L_MOUSE	P04430 homo sapien
10	424	40.0	108	1 KVIH_HUMAN	P01606 homo sapien
11	422	39.8	108	1 KVIH_HUMAN	P01594 homo sapien
12	448	39.5	108	1 KVIH_HUMAN	P01605 homo sapien
13	448	39.5	108	1 KVIH_HUMAN	P01668 mus musculus
14	446.5	39.3	110	1 KV3P_MOUSE	P01603 homo sapien
15	444	39.1	108	1 KVIH_HUMAN	P01611 homo sapien
16	444	39.1	108	1 KVIH_HUMAN	P01598 homo sapien
17	443	39.0	108	1 KVIH_HUMAN	P01607 homo sapien
18	443	39.0	108	1 KVIH_HUMAN	P01599 homo sapien
19	442	38.9	108	1 KVIH_HUMAN	P80362 homo sapien
20	441	38.9	108	1 KVIH_HUMAN	P01610 homo sapien
21	439	38.7	108	1 KVIH_HUMAN	P01608 homo sapien
22	438	38.6	108	1 KVIH_HUMAN	P01604 homo sapien
23	437	38.5	108	1 KVIH_HUMAN	P01593 homo sapien
24	431	38.0	108	1 KVIH_HUMAN	P01612 homo sapien
25	430.5	37.9	109	1 KVIH_HUMAN	P01596 homo sapien
26	429.5	37.8	107	1 KVIH_HUMAN	P01660 mus musculus
27	429	37.8	111	1 KV3H_MOUSE	P01609 homo sapien
28	425	37.4	108	1 KVIQ_HUMAN	P01595 homo sapien
29	423	37.3	108	1 KVIH_HUMAN	P01662 mus musculus
30	420	37.0	111	1 KV3J_MOUSE	P04432 homo sapien
31	419	36.9	129	1 KVIH_HUMAN	P01661 mus musculus
32	415	36.6	131	1 KV3I_MOUSE	P01663 mus musculus
33	411	36.2	111	1 KV3K_MOUSE	

ALIGNMENTS

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72189439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=61042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RT	(In) Franek P., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

P01625 homo sapien
P06314 homo sapien
P01670 mus musculus
P01671 mus musculus
P01613 homo sapien
P01659 mus musculus
P01658 mus musculus
P01602 homo sapien
P18135 homo sapien
P01673 mus musculus
P01620 homo sapien

34 410 36.1 114 1 KV4A_HUMAN
35 410 36.1 134 1 KV4C_HUMAN
36 404 35.6 111 1 KV3R_MOUSE
37 404 35.6 111 1 KV3S_MOUSE
38 404 35.6 112 1 KVIU_HUMAN
39 404 35.6 112 1 KV3G_MOUSE
40 404 35.6 132 1 KV3F_MOUSE
41 402 35.4 117 1 KVIJ_HUMAN
42 400.5 35.3 129 1 KV3L_HUMAN
43 399.5 35.2 129 1 KV3M_MOUSE
44 399 35.2 111 1 KV3U_MOUSE
45 396.5 34.9 109 1 KV3B_HUMAN

OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01937; KWS43.
DR HSSP; P80362; 1WT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 38
FT DOMAIN 39 53
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 54 60
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 41.1%; Score 467; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 4.1e-32;
Matches 86; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
DB 1 DIVLTQSPASLAVSLGQRTISCRASQSDVDGDSYNNWYQKPKGQPPKLLIYAASNLE 60

QY 61 GVPFRFSGSGGTDFTLTISSLPQEDFATYCCQSHEDPYTFGGTKVEIK 111
DB 61 GIPARFSGSGGTDFTLNIHPVEEDAATYCCQSNEDPPTFGSGTKLEIK 111

RESULT 4
ID KVIE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01865; K1HDE.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.

FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 40.8%; Score 463; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 8.4e-32;
Matches 89; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
DB 1 BIZMTQSPSSLSASVGDRTVITCRAGQSV----NKYLNWYQKPKAKVLIIFRASSLS 56

QY 61 GVPFRFSGSGGTDFTLTISSLPQEDFATYCCQSHEDPYTFGGTKVEIK 112
DB 57 GVPFRFSGSGGTDFTLTISSLPQEDFATYCCQSYTTPYTFGGTKVEMTR 108

RESULT 5
ID KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KWS08.
DR HSSP; P80362; 1WT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 38
FT DOMAIN 39 53
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 54 60
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 40.7%; Score 462; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.1e-31;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
DB 1 DIVLTQSPASLAVSLGQRTISCRASQSDVDGDSYNNWYQKPKGQPPKLLIYTANLSE 60

QY 61 GVPFRFSGSGGTDFTLTISSLPQEDFATYCCQSHEDPYTFGGTKVEIK 111
DB 61 GIPARFSGSGGTDFTLNIHPVEEDAATYCCQSNEDPPTFGSGTKLEIK 111

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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC DR PIR; A01883; KIHUWK.
CC DR HSSP; P01607; IREI.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; P:antigen binding; NAS.
CC DR GO; GO:0005955; P:immune response; NAS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 22 IG KAPPA CHAIN V-I REGION WALKER.
CC FT CHAIN 23 129 FRAMEWORK-1.
CC FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 46 56 FRAMEWORK-2.
CC FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 72 78 FRAMEWORK-3.
CC FT DOMAIN 79 110 FRAMEWORK-4.
CC FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 120 129 FRAMEWORK-4.
CC FT DISULFID 45 110 BY SIMILARITY.
CC FT NON_TER 129 129
CC SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 129;
Best Local Similarity 82.0%; Pred. No. 1.9e-31;
Matches 91; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSLASVGRVTITCRASQSDYDGDSDYNNWYQKPKKLLIYAASVLES 60
Db 23 DIQMTQSPSLASVGRVTITCRASQSI-----SNYLNWYQKPKKLLIYAASVLES 78
Qy 61 GVPESRSGSGGDFLTITSSLPQEDFATYCCQSHEDPYTFQGQTKVEIK 111
Db 79 GVTSRFSGSGGDFLTITSSLPQEDATYCCQSYSTLITFGQGTFLSIK 129

RESULT 8
KV3Q MOUSE STANDARD; PRT; 111 AA.
AC P01659;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; F01937; KMS69.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.

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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC DR PIR; A01883; KIHUWK.
CC DR HSSP; P01607; IREI.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; P:antigen binding; NAS.
CC DR GO; GO:0005955; P:immune response; NAS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 22 IG KAPPA CHAIN V-I REGION WALKER.
CC FT CHAIN 23 129 FRAMEWORK-1.
CC FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 46 56 FRAMEWORK-2.
CC FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 72 78 FRAMEWORK-3.
CC FT DOMAIN 79 110 FRAMEWORK-4.
CC FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 120 129 FRAMEWORK-4.
CC FT DISULFID 45 110 BY SIMILARITY.
CC FT NON_TER 129 129
CC SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.5e-31;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSLASVGRVTITCRASQSDYDGDSDYNNWYQKPKKLLIYAASVLES 60
Db 1 DIVLTQSPASVSLQRTATISCKASQSDYDGDSDYNNWYQKPKKLLIYAASVLES 60
Qy 61 GVPESRSGSGGDFLTITSSLPQEDFATYCCQSHEDPYTFQGQTKVEIK 111
Db 61 GIPARESGSGGDFLTINHPVEEDATYCCQSNEDPLTFGAGTKLELK 111

RESULT 7
KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
KW
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FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 40.4%; Score 459; DB 1; Length 111;
Best Local Similarity 75.7%; Pred. No. 1.9e-31;
Matches 84; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPKQPPKVLIPAASNLE 60

Qy 61 GVPFRFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 111
Db 61 GIPARFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 111

RESULT 9
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region C3P3 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79013520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PIR; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 40.1%; Score 455; DB 1; Length 111;
Best Local Similarity 75.7%; Pred. No. 4e-31;
Matches 84; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPKQPPKVLIPAASNLE 60

Qy 61 GVPFRFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 111
Db 61 GIPARFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 111

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Db 61 GIPARFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 111

RESULT 10
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78 (1986).
DR PIR; A01878; KIHUEN.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PIR; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944F96FD37 CRC64;

Query Match 40.0%; Score 454; DB 1; Length 108;
Best Local Similarity 81.2%; Pred. No. 4.7e-31;
Matches 91; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDGDSYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDVDGDSYNNWYQKPKAPKSLIYDASTLOS 56

Qy 61 GVPFRFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKLEIK 112
Db 57 GVPFRFSGSGSGTDFTLNHPVEEDAATYYCQSNEDPPTFGSGTKVQIKR 108

RESULT 11
KV1N_HUMAN
ID KV1N_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy

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PIR; A91653; K1HUAV.
PDB; 1UV5; 30-JAN-02.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin v region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT DOMAIN 24 34
FT FRAMEWORK-2.
FT DOMAIN 35 49
FT FRAMEWORK-3.
FT DOMAIN 50 56
FT FRAMEWORK-4.
FT DOMAIN 57 88
FT FRAMEWORK-5.
FT DOMAIN 89 97
FT FRAMEWORK-6.
FT DISULFID 98 107
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187B6F6FB9 CRC64;

Query Match 39.5%; Score 448; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 1.5e-30;
Matches 89; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVSGDRVITCRASQSDYDGDSDYMMVYQKPGKAPKLLIYAASYLE 60
DB 1 DIQMTQSPSSLSASVSGDRVITCRASQDI-----SDLNWYQKPGKAPKLLIYDASNLES 56

QY 61 GVPFRFSGSGSGTFTLTISLQPEFATYCCQSHEDPYTFGGQTKVEIKR 112
DB 57 GVPFRFSGSGSGAFTFTISLQPEDIATYCCQYDYLETFGGQTKVEIKR 108

RESULT 13
KVIM_HUMAN
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities";
RL Spec. J. Immunol. 5:677-684 (1976).
CC -|- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Igv; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT DOMAIN 24 34
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FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 39.5%; Score 448; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.5e-30;
Matches 88; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSTLSVSGDRVTITCRASQNV---NAYLNWYQKPGKAPKLLIYGASTREA 56

Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQTKVEIKR 112
Db 57 GVPFRFSGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQTKVEIKR 108

RESULT 14
KV3P MOUSE
ID KV3P MOUSE STANDARD; PRT; 110 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 39.3%; Score 445.5; DB 1; Length 110;
Best Local Similarity 75.7%; Pred. No. 2e-30;
Matches 84; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSLDYDGDSDYNNWYQKPGQPPKLLIYAASNL 60

Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQTKVEIK 111
Db 61 GIPARFSGSGSGTDFTLTINHPVEDAATYCHQS-EDPMTFGSGTKLEIK 110
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RESULT 15
KV1K HUMAN
ID KV1K HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSP; P80362; 1WTL.
DR PIR; A01869; KIHUKA.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 39.1%; Score 444; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.2e-30;
Matches 84; Conservative 14; Mismatches 10; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSTLSVSGDRVTITCRASQTV---LSVLNWYQKPGKAPKLLIYAASLET 56

Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQTKVEIKR 112
Db 57 GVPFRFSGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQTKVEIKR 108

Search completed: May 13, 2004, 15:45:56
Job time : 6.82265 secs
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:36:43 ; Search time 23.392 Seconds
(without alignments)
2940.454 Million cell updates/sec

Title: US-09-925-179-9

Perfect score: 1135

Sequence: 1 DIQTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	988	87.0	234	4 Q72473	Q72473 homo sapien
2	988	87.0	236	4 Q723Y4	Q723Y4 homo sapien
3	892.5	78.6	239	4 Q8NEK0	Q8NEK0 homo sapien
4	891.5	78.5	239	4 Q8TCD0	Q8TCD0 homo sapien
5	738	65.0	234	11 Q8R062	Q8R062 mus musculu
6	738	65.0	236	11 Q8TMD3	Q8TMD3 mus musculu
7	733	64.5	234	11 Q91WF8	Q91WF8 mus musculu
8	732	64.5	233	11 Q91WS9	Q91WS9 mus musculu
9	731	64.4	214	11 Q91IA5	Q91IA5 mus musculu
10	730	64.3	234	11 Q8VCP0	Q8VCP0 mus musculu
11	723	63.7	236	11 Q7TS98	Q7TS98 mus musculu
12	703.5	62.0	238	11 Q99M37	Q99M37 mus musculu
13	693.5	61.1	238	11 Q8VC16	Q8VC16 mus musculu
14	693.5	61.1	239	11 Q8VCS5	Q8VCS5 mus musculu
15	689.5	60.7	235	11 Q7TMK0	Q7TMK0 mus musculu
16	684.5	60.3	235	11 Q91W12	Q91W12 mus musculu

ALIGNMENTS

RESULT 1

ID	Q72473	PRELIMINARY;	PRT;	234 AA.
AC	Q72473;			
DT	01-OCT-2003 (T-EMBLrel. 25, Created)			
DT	01-OCT-2003 (T-EMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fehey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences";			
RP	proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			

Q8K0F8 mus musculu
Q8R028 mus musculu
Q7SZ36 xenopus lae
Q9UL77 homo sapien
Q96A9 homo sapien
Q96A6 homo sapien
Q9UL81 homo sapien
Q9UL70 homo sapien
Q8NEJ1 homo sapien
Q8ILU6 mus musculu
Q8WUK4 homo sapien
Q8TBC9 homo sapien
Q8WTU6 homo sapien
Q9UL79 homo sapien
Q8N355 homo sapien
Q8NSF4 homo sapien
Q920E9 mus musculu
Q96E61 homo sapien
Q7Z2U7 homo sapien
Q99M11 mus musculu
Q7Z2U3 homo sapien
Q8WUK3 homo sapien
Q9GYF0 mus musculu
Q8K1F3 mus musculu
Q8K1F1 mus musculu
Q9UL78 homo sapien
Q920E6 mus musculu
Q8K1F2 mus musculu
Q9UL83 homo sapien

```

RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match
Best Local Similarity 87.0%; Score 988; DB 4; Length 234;
Matches 193; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY 2 IQLTQSPSSLSASVGDRTVITCRASQSVVDYDGSYMWYQOKPGKAPKLLIYAASYLESG 61
DB 22 IRMTQSPSSFSASTGDRVTITCRASQSI-----GSYLAWYQOKPGKAPQLLIYAASLTQSG 77
QY 62 VPSRFSGSGSGTDTLTLSISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVFI 121
DB 78 VPSRFSGSGSGTDTLTLSISLQSEDFAFYCQYTYTFWFGQGTKEIKRTVAAPSVFI 137
QY 122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSLSS 181
DB 138 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSLSS 197
QY 182 TLTLTKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 198 TLTLTKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 2
Q723Y4
ID Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichmond J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maizra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match
Best Local Similarity 87.0%; Score 988; DB 4; Length 236;
Matches 193; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match
Best Local Similarity 87.0%; Score 988; DB 4; Length 234;
Matches 193; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY 2 IQLTQSPSSLSASVGDRTVITCRASQSVVDYDGSYMWYQOKPGKAPKLLIYAASYLESG 61
DB 22 IRMTQSPSSFSASTGDRVTITCRASQSI-----GSYLAWYQOKPGKAPQLLIYAASLTQSG 77
QY 62 VPSRFSGSGSGTDTLTLSISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVFI 121
DB 78 VPSRFSGSGSGTDTLTLSISLQSEDFAFYCQYTYTFWFGQGTKEIKRTVAAPSVFI 137
QY 122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSLSS 181
DB 138 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSLSS 197
QY 182 TLTLTKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 198 TLTLTKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 3
Q8NEKO
ID Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40357; S40357.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SMC0407; IG1; 1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match
Best Local Similarity 78.6%; Score 892.5; DB 4; Length 239;
Matches 173; Conservative 17; Mismatches 28; Indels 1; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSVVDY-DGDSYMWYQOKPGKAPKLLIYAASYLE 59
DB 21 DIVMTQSPLSLPTVTPGPASISCRSSQSLHSDGYNYLDWYLOKPGSQPLLIIYLSNRA 80
QY 60 SGVPSRFSGSGSGTDTLTLSISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSV 119
DB 81 SGVPSRFSGSGSGTDTLTLSISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSV 140
QY 120 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSL 179
DB 141 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQSGNSQSVTEQDSKDYSL 200
QY 180 SSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 218
DB 201 SSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

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RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
ID Q8TCD0;
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, SC022362; RAH22362.1; -.
DR PIR, S34095; S34095.
DR PIR, S42267; S42267.
DR PIR, S42268; S42268.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 78.5%; Score 891.5; DB 4; Length 239;
Best Local Similarity 77.2%; Pred. No. 2.1e-73;
Matches 169; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDY-DGDSYNNWYQKPGKAPKLLIYAASYLE 59
DB 21 DVVMTQSPLSPLVTILGQPASISCRSTQSLVSDGNTYLNWFGQRPQSPRELIYKVSNRD 80
QY 60 SGVPRFSGSGGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSV 119
DB 81 SGVPRFSGSGGTDFTLKTRVEAEDVGVEFCMQGTHMPSTFGGTKLEIKRTVAAPSV 140
QY 120 FIFPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179
DB 141 FIFPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200
QY 180 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
Q8R062 PRELIMINARY; PRT; 234 AA.
ID Q8R062;
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC027418; RAH27418.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C91426AEB1 CRC64;

Query Match 65.0%; Score 738; DB 11; Length 234;
Best Local Similarity 64.2%; Pred. No. 2.2e-59;
Matches 140; Conservative 29; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
DB 21 DIQMTTTSLSASLGDRTITCSASQGI----SNLYNNYQKPGDGTVKLLIYTSLSLS 76
QY 61 GVPSPFSGSGGTDFTLTISLQPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSV 120
DB 77 GVPSPFSGSGGTHTYSLTISNLEPEDATYYCQYSPFPTFGSGTKLEIKADAAPTVS 136
QY 121 FIFPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 137 FIFPSPDEQLTSGGASVVCFLNNFYPRKIDSGSQNGVLSWTDQDSKDSYSL 196
QY 181 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 197 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 6
Q7TMK3 PRELIMINARY; PRT; 236 AA.
ID Q7TMK3;
AC Q7TMK3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC055906; AAH55906.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03489AAA6396F CRC64;

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DR EMBL; AF152371; AAD40242.1; --
 DR PDB; 1CIC; 11-MAR-03.
 DR PDB; 1E08; 29-NOV-00.
 DR PDB; 1K6Q; 18-DEC-02.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_MHC.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1
 FT 214 214
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 64.4%; Score 731; DB 11; Length 214;
 Best Local Similarity 63.3%; Pred. No. 8.6e-59;
 Matches 138; Conservative 31; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSMYASLGERTITCKASQDI---NSYLSWFOQKPGKSPKLLIYRANRLVD 56

QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
 DB 57 GVPSRFGSGSGQDYSLTISSEYEDMGIIYCLQYDFPFPGSGTKLEIKRADAAPTVS 116

QY 121 IFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYSL 180
 DB 117 IFPPSDEQLTSGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 176

QY 181 STLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
 DB 177 STLTLTCKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 214

RESULT 10

Q8VCP0 PRELIMINARY; PRT; 234 AA.

ID Q8VCP0
 AC Q8VCP0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019474; AAH19474.1; --
 DR PIR; B47329; B47329.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 64.3%; Score 730; DB 11; Length 234;
 Best Local Similarity 63.8%; Pred. No. 1.2e-58;
 Matches 139; Conservative 29; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
 DB 21 DIQLTQSPASLSVGETTITCRASNI-----YSYLAWYQKQKSGQLLVYNAKTLD 76

QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
 DB 77 GVPSRFGSGSGTDFSLKINSLOPEDFGSYGHHSGIPFTFGSGTKLEIKRADAAPTVS 136

QY 121 IFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYSL 180
 DB 137 IFPPSDEQLTSGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 196

QY 181 STLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
 DB 197 STLTLTCKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 234

RESULT 11

Q7TS98 PRELIMINARY; PRT; 236 AA.

ID Q7TS98
 AC Q7TS98;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-colorectal carcinoma light chain.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93383497; PubMed=8372513;
 RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
 RT "Cloning and characterization of 1116NS19.9 heavy and light chain
 cDNAs and expression of antibody fragments in *Escherichia coli*."
 RL Year Immunol. 7:56-62(1993).
 DR EMBL; S65921; AAB28160.1; --
 SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

Query Match 63.7%; Score 723; DB 11; Length 236;
 Best Local Similarity 62.8%; Pred. No. 5.3e-58;
 Matches 137; Conservative 32; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNYQKPGKAPKLLIYAASYLE 60
 DB 23 DIKMTQSPSSMYASLGERTITCKASQDI---NSYLSWFOQKPGKSPKLLIYRANRLVD 78

QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGQTKVEIKRTVAAPSVF 120
 DB 79 GVPSRFGSGSGQDYSLTISSEYEDMGIIYCLQYDFPFPGSGTKLEIKRADAAPTVS 138

QY 121 IFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYSL 180
 DB 139 IFPPSDEQLTSGASVVCVCLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 198

QY 181 STLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
 DB 199 STLTLTCKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 236

RESULT 12

Q99M37 PRELIMINARY; PRT; 238 AA.

ID Q99M37
 AC Q99M37;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002035; AAH02035.1; --

Search completed: May 13, 2004, 15:47:22
Job time : 24.392 secs